

STIC-Biotech/ChemLib

From: Chan, Christina
Sent: Tuesday, August 27, 2002 1:43 PM
To: Davis, Minh-Tam; STIC-Biotech/ChemLib
Subject: RE: Rush search request for 09/583848

Please rush. Thanks Chris

-----Original Message-----

From: Davis, Minh-Tam
Sent: Tuesday, August 27, 2002 1:25 PM
T : Chan, Christina
Subject: Rush search request for 09/583848

Please use the grandparent cases 08/967727 or 08/037230 for search
Please search in commercial database and in issued patent files:

1) Nucleotides 451-1156 of SEQ ID NO:18

Thank you.

MINH TAM DAVIS

ART UNIT 1642, ROOM 8A01, MB 8E12
305-2008

Minh-Tam,
Seq ID 18, SN 08/967727 (Pat. no.
6025474) only 225 residues

Beverly
IEOS
C8-4994

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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SEARCH REQUEST FORM

Requestor's

Name: _____

Serial

Number: _____

Date: _____

Phone: _____

Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 09-05-02

Searcher: Beverly e4994

Terminal time: 20

Elapsed time: _____

CPU time: _____

Total time: 23

Number of Searches: _____

Number of Databases: 1

Search Site

_____ STIC

_____ CM-1

_____ Pre-S

Type of Search

_____ N.A. Sequence

_____ A.A. Sequence

_____ Structure

_____ Bibliographic

Vendors

_____ IG

_____ STN

_____ Dialog

_____ APS

_____ Geninfo

_____ SDC

_____ DARC/Questel

☒ Other CGN

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Davis, M.
09/583848
Seq-ID 18

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 4, 2002, 11:13:22 ; Search time 1922.63 Seconds
(without alignments)
2448.974 Million cell updates/sec

Title: US-08-967-727-18
Perfect score: 225
Sequence: 1 TATTTCTTTCCCTGTGATCTT.....GGCACTGTGCCCTGAGGAG 225

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pi.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	100.0%	Score 225;	DB 6;	Length 225;

1	225	100.0	225	6	AR153509	Sequence 18	225 bp	DNA	linear	PAT 08-AUG-2001
2	225	100.0	225	6	I36933	Sequence 18				
3	220.2	97.9	945	6	AR167371	Sequence 18				
4	220.2	97.9	945	6	HSU10339	Human				
5	220.2	97.9	1019	6	AR167377	Sequence 18				
6	220.2	97.9	1019	9	HUMMAGEB	Sequence 18				
7	220.2	97.9	1362	6	AX019384	Human				
8	220.2	97.9	3871	9	HSU10691	Human				
9	220.2	97.9	245077	9	AF002997	Homo sapi				
10	213.8	95.0	1212	6	AX019380	Sequence 18				
11	213.8	95.0	1353	6	AX019376	Sequence 18				
12	213.8	95.0	1569	6	AX343855	Sequence 18				
13	213.8	95.0	1640	6	AR153502	Sequence 18				
14	213.8	95.0	1640	6	I36926	Sequence 11				
15	213.8	95.0	1663	9	BC011744	Homo sapi				
16	213.8	95.0	1709	9	BC000340	Homo sapi				
17	213.8	95.0	1710	9	BC017389	Homo sapi				
18	213.8	95.0	1715	9	BC016803	Homo sapi				
19	213.8	95.0	1753	9	BC005963	Homo sapi				
20	213.8	95.0	4204	6	AR079453	Sequence 18				
21	213.8	95.0	4204	6	AR167370	Sequence 18				
22	213.8	95.0	4204	6	AR170361	Sequence 18				
23	213.8	95.0	4204	6	AX333265	Sequence 18				
24	213.8	95.0	4204	9	HS003735	Human				
25	213.8	95.0	245077	9	AF002997	Homo sapi				
26	213.8	95.0	289248	9	U82671	Homo sapi				
27	196.8	87.5	1678	9	BC003408	Homo sapi				
28	195.2	86.8	727	6	AX328164	Sequence 18				
29	195.2	86.8	1030	6	AX328166	Sequence 18				
30	195.2	86.8	4157	6	AR153500	Sequence 18				
31	195.2	86.8	4157	6	I36924	Sequence 9				
32	195.2	86.8	4523	6	AX119704	Sequence 18				
33	195.2	86.8	4523	9	HUMMAGE12X	Sequence 18				
34	195.2	86.8	4559	9	AR167369	Sequence 18				
35	195.2	86.8	4559	9	HUMMAGE2X	Sequence 18				
36	195.2	86.8	289248	9	U82671	Homo sapi				
37	195.2	86.8	302250	6	AX335531	Sequence 18				
38	195.2	86.8	302250	6	AX335531	Sequence 18				
39	193.6	86.0	1657	9	BC013098	Homo sapi				
40	192	85.3	3295	2	AC084372	Sequence 18				
41	184	81.8	951	9	AF443295	Homo sapi				
42	163.2	72.5	1084	6	AR052774	Sequence 18				
43	163.2	72.5	1094	6	AR052773	Sequence 18				
44	163.2	72.5	1338	6	AX019382	Sequence 18				
45	163.2	72.5	1341	6	AX019377	Sequence 18				

ALIGNMENTS

RESULT 1	AR153509	Sequence 18 from patent US 6235525.	225 bp	DNA	linear	PAT 08-AUG-2001
LOCUS	AR153509	Sequence 18 from patent US 6235525.				
DEFINITION	AR153509	Sequence 18 from patent US 6235525.				
ACCESSION	AR153509	Sequence 18 from patent US 6235525.				
VERSION	AR153509.1	GI:15121041				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 225)					
AUTHORS	van den Eynde,B., van der Bruggen,P. and Boon-Falleur,T.					
TITLE	Isolated nucleic acid molecules coding for tumor rejection antigen precursor MAGE-3 and uses thereof					
JOURNAL	Patent: US 6235525-A 18 22-MAY-2001;					
FEATURES	location/Qualifiers					
source	1..225					
BASE COUNT	44 a 65 c 58 g 58 t					
ORIGIN	/organism="unknown"					

Query Match 100.0%; Score 225; DB 6; Length 225;

Best Local Similarity 100.0%; Pred. No. 5.3e-43; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60
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QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGCTGTACATCTTTGGCACCTGCTGGGCCTC 120
|||||
Db 61 GAGCTGATGGAAGTGGACCCCATCGGCACGCTGTACATCTTTGGCACCTGCTGGGCCTC 120
|||||

QY 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTGTATATC 180
|||||
Db 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTGTATATC 180
|||||

QY 181 ATCCTGGCCATAATCGCAAGAGAGGGGACCTGTGCCCTGTAGGAG 225
|||||
Db 181 ATCCTGGCCATAATCGCAAGAGAGGGGACCTGTGCCCTGTAGGAG 225
|||||

RESULT 2
LOCUS I36933 225 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 18 from patent US 5612201.
ACCESSION I36933
VERSION I36933.1 GI:2084893
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 225)
AUTHORS De Plaen,E., Boon-Falleur,T., Lethe,B., Szikora,J.-P., De Smet,C.
and Chomez,P.
TITLE Isolated nucleic acid molecules useful in determining expression of
a tumor rejection antigen precursor
JOURNAL Patent: US 5612201-A 18 18-MAR-1997;
FEATURES Location/Qualifiers
source 1..225
BASE COUNT 44 a 65 c 58 g 58 t
ORIGIN

Query Match 100.0%; Score 225; DB 6; Length 225;
Best Local Similarity 100.0%; Pred. No. 5.3e-43;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60
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Db 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60
|||||

QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGCTGTACATCTTTGGCACCTGCTGGGCCTC 120
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Db 61 GAGCTGATGGAAGTGGACCCCATCGGCACGCTGTACATCTTTGGCACCTGCTGGGCCTC 120
|||||

QY 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTGTATATC 180
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Db 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTGTATATC 180
|||||

QY 181 ATCCTGGCCATAATCGCAAGAGAGGGGACCTGTGCCCTGTAGGAG 225
|||||
Db 181 ATCCTGGCCATAATCGCAAGAGAGGGGACCTGTGCCCTGTAGGAG 225
|||||

RESULT 3
LOCUS AR167371 945 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 7 from patent US 6287569.
ACCESSION AR167371
VERSION AR167371.1 GI:17903147
KEYWORDS
SOURCE
ORGANISM
Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 945)
AUTHORS Kipps,T.J. and Wu,Y.
TITLE Vaccines with enhanced intracellular processing
JOURNAL Patent: US 6287569-A 7 11-SEP-2001;
FEATURES Location/Qualifiers
source 1..945
BASE COUNT 213 a 254 c 275 g 203 t
ORIGIN

Query Match 97.9%; Score 220.2; DB 6; Length 945;
Best Local Similarity 98.7%; Pred. No. 6.9e-42;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60
|||||
Db 433 TACTTCTTCTGTGATCTTCAGCAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 492
|||||

QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGCTGTACATCTTTGGCACCTGCTGGGCCTC 120
|||||
Db 493 GAGCTGATGGAAGTGGACCCCATCGGCACGCTGTACATCTTTGGCACCTGCTGGGCCTC 552
|||||

QY 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTGTATATC 180
|||||
Db 553 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTGTATATC 612
|||||

QY 181 ATCTGTGCCATAATCGCAAGAGAGGGGACCTGTGCCCTGTAGGAG 225
|||||
Db 613 ATCTGTGCCATAATCGCAAGAGAGGGGACCTGTGCCCTGTAGGAG 657
|||||

RESULT 4
LOCUS HSU10339 945 bp mRNA linear PRI 13-JUN-1994
DEFINITION Human MAGE-3b mRNA, complete cds.
ACCESSION U10339
VERSION U10339.1 GI:499121
KEYWORDS
SOURCE
ORGANISM
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 945)
AUTHORS Fenton,R.G.
TITLE Cloning and Analysis of MAGE-1 Related Genes
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 945)
AUTHORS Fenton,R.G.
TITLE Direct Submission
JOURNAL Submitted (03-JUN-1994) Robert G. Fenton, BRMP, NCI-FCRDC,
Frederick, MD 21702, USA
FEATURES Location/Qualifiers
source 1..945
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MAGE-3b"
/haplotype="HLA-A1/A2"
/cell_line="DM150"
/cell_type="melanoma"
/tissue_type="skin"
/clone_lib="DM150 library"
/dev_stage="adult"
/note="cancer patient"
1..945
/codon_start=1
/product="MAGE-3b"
/protein_id="AA19006.1"
/db_xref="GI:499122"

CDS
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SEFQAALSRKVKLVHFLLLKYRAREPVTKAEMLGSVVGNQYFPFVIFSKASDQLQ

VFQIEMVEDPIGHVYIFATCLGLSYDGLLDNQIMPKTGFLLIILAIITAKEGDCAPE
EKIMELSVLEVEGREDISFGDPKLLQYFVOENYLEYRQVPGSDPACYEFLWGR
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BASE COUNT 213 a 254 c 275 g 203 t
ORIGIN

Query Match 97.9%; Score 220.2; DB 9; Length 945;
Best Local Similarity 98.7%; Pred. No. 6.9e-42;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTCTTCTTCCTGTGATCTTCAGCAAGCTTCGGATTCCTTGACGTGGTCTTTGGCATC 60
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Db 433 TACTTCTTCTTCCTGTGATCTTCAGCAAGCTTCGGATTCCTTGACGTGGTCTTTGGCATC 492
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QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCCTGGGCCTC 120
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Db 493 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCCTGGGCCTC 552
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QY 121 TCCTACGATGGCTGCTGGGTGACATCAGATCATGCCACGACAGGCTTCCTGTATAATC 180
|||
Db 553 TCCTACGATGGCTGCTGGGTGACATCAGATCATGCCACGACAGGCTTCCTGTATAATC 612
|||
QY 181 ATCTGGCCATATCCAGAGAGGGCGACTGTGCCCTCGAGGAG 225
|||
Db 613 ATCTGGCCATATCCAGAGAGGGCGACTGTGCCCTCGAGGAG 657
|||

RESULT 5
AR167377
LOCUS AR167377 1019 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 13 from patent US 6287569.
ACCESSION AR167377
VERSION AR167377.1 GI:17903153
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1019)
AUTHORS Kipps, T.J. and Wu, Y.
TITLE Vaccines with enhanced intracellular processing
JOURNAL Patent: US 6287569-A 13 11-SEP-2001;
FEATURES Location/Qualifiers
source
1..1019
/organism="unknown"

BASE COUNT 224 a 284 c 292 g 219 t
ORIGIN

Query Match 97.9%; Score 220.2; DB 6; Length 1019;
Best Local Similarity 98.7%; Pred. No. 6.9e-42;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTCTTCTTCCTGTGATCTTCAGCAAGCTTCGGATTCCTTGACGTGGTCTTTGGCATC 60
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Db 498 TACTTCTTCTTCCTGTGATCTTCAGCAAGCTTCGGATTCCTTGACGTGGTCTTTGGCATC 557
|||
QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCCTGGGCCTC 120
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Db 558 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCCTGGGCCTC 617
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QY 121 TCCTACGATGGCTGCTGGGTGACATCAGATCATGCCACGACAGGCTTCCTGTATAATC 180
|||
Db 618 TCCTACGATGGCTGCTGGGTGACATCAGATCATGCCACGACAGGCTTCCTGTATAATC 677
|||
QY 181 ATCTGGCCATATCCAGAGAGGGCGACTGTGCCCTCGAGGAG 225
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Db 678 ATCTGGCCATATCCAGAGAGGGCGACTGTGCCCTCGAGGAG 722
|||

RESULT 6
HUMMAGEB HUMMAGEB
LOCUS HUMMAGEB 1019 bp mRNA linear PRI 07-FEB-1999

DEFINITION Human mRNA for MAGE-6 protein, complete cds.
ACCESSION D32076
VERSION D32076.1 GI:1125015
KEYWORDS MAGE-6 protein; melanoma antigen.
SOURCE Homo sapiens cell-line M73 CDNA to mRNA.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1019)
AUTHORS Imai, Y.
TITLE Direct Submission
JOURNAL Submitted (08-JUL-1994) Yasuhisa Imai, Kurume University School of Medicine, Immunology; Asahi 67, Kurume, Fukuoka 830, Japan
(Tel:0942-31-7551, Fax:0942-31-7699)

REFERENCE 2 (bases 1 to 1019)
AUTHORS Imai, Y., Shichijo, S., Yamada, A., Katayama, T., Yano, H. and Itoh, K.
TITLE Sequence analysis of the MAGE gene family encoding human tumor-rejection antigens
JOURNAL Gene 160 (2), 287-290 (1995)
MEDLINE 95369706
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="M73"
66..1010
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/note="Nomenclature of MAGE-6 was according to MAGE gene's 27 nucleotide sequences of HLA-A1 binding motif (Traversari et al., 1992)"
/codon_start=1
/evidence=experimental
/product="MAGE-6 protein"
/protein_id="BA06842.1"
/db_xref="GI:1125016"
/translation="MPLEQRSQCKPEEGLEARGEALGLVGAQAPATEQEASST
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VFQIEMVEDPIGHVYIFATCLGLSYDGLLDNQIMPKTGFLLIILAIITAKEGDCAPE
EKIMELSVLEVEGREDISFGDPKLLQYFVOENYLEYRQVPGSDPACYEFLWGR
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CDS

BASE COUNT 224 a 284 c 292 g 219 t
ORIGIN

Query Match 97.9%; Score 220.2; DB 9; Length 1019;
Best Local Similarity 98.7%; Pred. No. 6.9e-42;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTCTTCTTCCTGTGATCTTCAGCAAGCTTCGGATTCCTTGACGTGGTCTTTGGCATC 60
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Db 498 TACTTCTTCTTCCTGTGATCTTCAGCAAGCTTCGGATTCCTTGACGTGGTCTTTGGCATC 557
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QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCCTGGGCCTC 120
|||
Db 558 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCCTGGGCCTC 617
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QY 121 TCCTACGATGGCTGCTGGGTGACATCAGATCATGCCACGACAGGCTTCCTGTATAATC 180
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Db 618 TCCTACGATGGCTGCTGGGTGACATCAGATCATGCCACGACAGGCTTCCTGTATAATC 677
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QY 181 ATCTGGCCATATCCAGAGAGGGCGACTGTGCCCTCGAGGAG 225
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Db 678 ATCTGGCCATATCCAGAGAGGGCGACTGTGCCCTCGAGGAG 722
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RESULT 7
AX019384
LOCUS AX019384 1362 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 10 from Patent WO9940188.
ACCESSION AX019384
VERSION AX019384.1 GI:10043354
KEYWORDS

```

SOURCE          human.
ORGANISM         Homo sapiens
REFERENCE        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE           1 (bases 1 to 1362)
                Slaoui,M.M., Cohen,J., Cabezon,S.T. and Vinals,B.C.
                Tumor-associated antigen derivatives from the mage family, and
                nucleic acid sequences encoding them, used for the preparation of
                fusion proteins and of compositions for vaccination
                Patent: WO 9940188-A 10 12-AUG-1999;
                SLAOUI MONCEF MOHAMED (BE); SMITHKLINE BEECHAM BIOLOG (BE); COHEN
                JOSEPH (BE); CABEZON SILVA TERESA (BE); VINALS BASSOLS CARLOTA (BE)
FEATURES         Location/Qualifiers
                source          1..1362
                                /organism="Homo sapiens"
                                /db_xref="taxon:9606"
                                /note="Melanoma tissue"
BASE COUNT      345 a 348 c 383 g 286 t
ORIGIN
Query Match     97.9%; Score 220.2; DB 6; Length 1362;
Best Local Similarity 98.7%; Pred. No. 6.9e-42;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 823 TACTTCTTCTTGATCTTCAGCAAGCTTCGGAATTCCTGCAGCTGGTCTTTGGCATC 882
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QY 61 GAGCTGATGGAAGTGGACCCATCGCCACCTGTACATCTTTGCCACCTGCTGGCCCTC 120
    |||||||
DB 883 GAGCTGATGGAAGTGGACCCATCGCCACCTGTACATCTTTGCCACCTGCTGGCCCTC 942
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QY 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGCAGAGGCTTCTGTATAATC 180
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DB 943 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGCAGAGGCTTCTGTATAATC 1002
    |||||||
QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
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DB 1003 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 1047
    |||||||

RESULT 8
HSU10691        HSU10691        3871 bp  DNA  linear  PRI 23-JUN-1995
LOCUS           Human MAGE-6 antigen (MAGE6) gene, complete cds.
DEFINITION      U10691
ACCESSION       U10691
VERSION         U10691.1 GI:533522
KEYWORDS        human.
SOURCE          human.
ORGANISM        Homo sapiens
REFERENCE        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                1 (bases 1 to 3871)
                De Plaen,E., Arden,K., Traversari,C., Gaforio,J.J., Szikora,J.P.,
                De Smet,C., Brasseur,F., van der Bruggen,P., Lethe,B.,
                Lurquin,C.Brasseur.R., Chomez,P., De Backer,O., Cavenee,W. and
                Boon,T.
                Structure, chromosomal localization, and expression of 12 genes of
                the MAGE family
                Immunogenetics 40 (5), 360-369 (1994)
                95012457
                2 (bases 1 to 3871)
                De Plaen,E.
                Direct Submission
                Submitted (14-JUN-1994) Etienne De plaen, Ludwig Institute for
                Cancer Research, 74 Avenue Hippocrate, Brussels, 1200, Belgium
FEATURES         Location/Qualifiers
                source          1..3871
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                                /isolate="patient M22"
                                /db_xref="taxon:9606"
                                /chromosome="X"

/sex="female"
/cell_type="lymphocyte"
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/dev_stage="adult"
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/number=3
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/protein_id="AA68875.1"
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/translation="MPLEQRSHQKPEEGLEARGEALGLVGAQAPATEEOBAASSST
LV8VTLGEVPAAESPDPOGASSLPTTMYPLWSQSYEDSSNQEEGSPNPDLE
SEFQAALSRKAKLYHELLLKYRARFVTKAEMLGSVYGNWQYFFVFIFSKASDLSL
VFGIELMEVDPIGHVYIFATCLGSLDGLDNOIMPTKLTQYFVOENYLEYRQVPGSDPACYEFLWGP
EKIWEELSVLEFEGREDSIFGDPKLLTQYFVOENYLEYRQVPGSDPACYEFLWGP
ALietsyKVLHMHVTKISGGRISYPLLHEWALREGEE"
BASE COUNT      865 a 1050 c 1117 g 839 t
ORIGIN
Query Match     97.9%; Score 220.2; DB 9; Length 3871;
Best Local Similarity 98.7%; Pred. No. 6.7e-42;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTCTTCTTGATCTTCAGCAAGCTTCGGAATTCCTGCAGCTGGTCTTTGGCATC 60
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DB 2696 TACTTCTTCTTGATCTTCAGCAAGCTTCGGAATTCCTGCAGCTGGTCTTTGGCATC 2755
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QY 61 GAGCTGATGGAAGTGGACCCATCGCCACCTGTACATCTTTGCCACCTGCTGGCCCTC 120
    |||||||
DB 2756 GAGCTGATGGAAGTGGACCCATCGCCACCTGTACATCTTTGCCACCTGCTGGCCCTC 2815
    |||||||
QY 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGCAGAGGCTTCTGTATAATC 180
    |||||||
DB 2816 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGCAGAGGCTTCTGTATAATC 2875
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QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
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DB 2876 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 2920
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RESULT 9
AF002997        AF002997        245077 bp  DNA  linear  PRI 13-APR-2001
LOCUS           Homo sapiens chromosome X map Xq28, complete sequence.
DEFINITION      AF002997
ACCESSION       AF002997
VERSION         AF002997.2 GI:13621226
KEYWORDS        HTG; HTGS_ACTIVEFIN.
SOURCE          human.
ORGANISM        Homo sapiens
REFERENCE        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                1 (bases 9444 to 72299)
                Gloeckner,G., Rosenthal,A., Drescher,B., Schattevoy,R., Poustka,A.
                and Kioschis,P.
                Genomic sequence in Xq28
                Unpublished
                2 (bases 1 to 245077)
                Galoczky,P., Schillhabel,M., Rosenthal,A. and Platzter,M.
                Chromosome X genomic sequence
                Unpublished
                3 (bases 1 to 245077)
                Gloeckner,G., Rosenthal,A., Drescher,B. and Schattevoy,R.
                Direct Submission
                Submitted (07-MAY-1997) Genome Analysis, Institute of Molecular
                Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
                4 (bases 1 to 245077)
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AUTHORS      Platzer,M.
TITLE        Direct Submission
JOURNAL      Submitted (13-APR-2001) Genome Analysis, Institute of Molecular
              Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany
COMMENT      On Apr 13, 2001 this sequence version replaced gi:4409798.
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               /db_xref="taxon:9606"
               /chromosome="X"
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		Best Local Similarity 98.7%;	Pred. No. 6.3e-42;
Matches	222; Conservative	0; Mismatches	3; Indels
		Gaps	0;
QY	1 TATTCTTTCCGTGATCTTCAGCAAAAGCTTCCGATTCCTTGACAGCTGGCTTTTGGCATC	60	
Dbl	164120 TACTTCTTTCTCGTAGTCTTCAGCAAAAGCTTCCGATTCCTTGACAGCTGGCTTTTGGCATC	164179	
QY	61 GAGCTGATGAAGTGGACCCTCATGCCGCACGTGFACATCTTTGGCACCTGCCTGGGCCTC	120	
Dbl	164180 GAGCTGATGANAGTGGACCCTCATGCCGCACGTGFACATCTTTGGCACCTGCCTGGGCCTC	164239	
QY	121 TCCTACGATGCCCTGTGGTGGACAATCAGATCATGCCACAGCAGGCTTCTCGATAATC	180	
Dbl	164240 TCCTACGATGCCCTGTGGTGGACAATCAGATCATGCCAAGACAGGCTTCTCGATAATC	164299	
QY	181 ATCTGGCCATAATCGCAAGAGAGGGGACTGTGCCCTGAGGAG	225	
Dbl	164300 ATCTGGCCATAATCGCAAGAAGAGGGGACTGTGCCCTGAGGAG	164344	
RESULT	10		
AXO19380			PAT 07-SEP-2000
LOCUS	AXO19380	1212 bp	linear
DEFINITION	Sequence 6 from Patent WO9940188.		
ACCESSION	AXO19380		
VERSION	AXO19380.1 GI:10043352		
KEYWORDS	human.		
SOURCE	Homo sapiens		
ORGANISM	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1212)		
REFERENCE	Slauoui,M.M., Cohen,J.J., Cabezon,S.T. and Vinals,B.C.		
AUTHORS	Tumour-associated antigen derivatives from the mage family, and TITLE		

nucleic acid sequences encoding them, used for the preparation of fusion proteins and of compositions for vaccination
Patent: WO 9940188-A 6 12-AUG-1999;
SLAOUTI MONCEFF MOHAMED (BE); SMITHKLINE BEECHAM BIOLOG (BE); COHEN JOSEPH (BE); CABEZON SILVA TERESA (BE); VINALS BASSOLS CARLOTA (BE)

FEATURES
source
1. .1212
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Melanoma tissue"

BASE COUNT 289 a 319 c 344 g 260 t
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Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db 673 TATTCTTTCTGTGATCTTCAGCAAGCTTCCAGTCTCTTGACAGCTGGTCTTTGGCATC 732
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Qy 61 GAGCTGATGGAAGTGGACCCATCGGCACGCTGACATCTTTGCCACCTGCCTGGGCCTC 120
|||||
Db 733 GAGCTGATGGAAGTGGACCCATCGGCACCTGACATCTTTGCCACCTGCCTGGGCCTC 792
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Qy 121 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCACGAGCAGGCTTCCTGATATC 180
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Db 793 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCACGAGCAGGCTTCCTGATATC 852
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Qy 181 ATCTTGCCCAATAATCGCAAGAGGGCGACTGTGCCCTGAGGAG 225
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Db 853 GTCTGGCCATAATCGCAAGAGGGCGACTGTGCCCTGAGGAG 897
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RESULT 11
AX019376

LOCUS AX019376 1353 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 2 from Patent WO9940188.
ACCESSION AX019376
VERSION AX019376.1 GI:10043350
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1353)
SLAOUTI, M., Cohen, J., Cabezon, S.T. and Vinals, B.C.
Tumor-associated antigen derivatives from the mage family, and
nucleic acid sequences encoding them, used for the preparation of
fusion proteins and of compositions for vaccination
Patent: WO 9940188-A 2 12-AUG-1999;
SLAOUTI MONCEFF MOHAMED (BE); SMITHKLINE BEECHAM BIOLOG (BE); COHEN JOSEPH (BE); CABEZON SILVA TERESA (BE); VINALS BASSOLS CARLOTA (BE)

FEATURES
source
1. .1353
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Melanoma tissue"

BASE COUNT 342 a 337 c 354 g 320 t
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Best Local Similarity 96.9%; Pred. No. 2.2e-40;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TATTCTTTCTGTGATCTTCAGCAAGCTTCCGATTCTCTTGACAGCTGGTCTTTGGCATC 60
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Db 814 TATTCTTTCTGTGATCTTCAGCAAGCTTCCAGTCTCTTGACAGCTGGTCTTTGGCATC 873
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Qy 61 GAGCTGATGGAAGTGGACCCATCGGCACGCTGACATCTTTGCCACCTGCCTGGGCCTC 120
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Db	874	GAGCTGATGGGAAGTGGAGCCCATCGGCACATGTTGACATCTTTTGGCACACTGCTGGGCGCTC	933			
Qy	121	TCCTACGATGGCCCTGCTGGGTGACAATCAGATCATGCCCCAGGACAGGCTTCTCTGATAATC	180			
Db	934	TCCTACGATGGCCCTGCTGGGTGACAATCAGATCATGCCCCAGGACAGGCTTCTCTGATAATC	993			
Qy	181	ATCTGGCCATAATCGCAAGAGAGGGGACGTGTGCCCTGTAGAGG	225			
Db	994	GTCCTGGCCATAATCGCAAGAGAGGGGACGTGTGCCCTGTAGAGG	1038			
RESULT 12						
LOCUS	AX343855	1569 bp	linear			
DEFINITION	Sequence 1 from Patent WO0200892.					
ACCESSION	AX343855					
VERSION	AX343855.1	GI:18491925				
KEYWORDS	synthetic construct.					
SOURCE	artificial sequence.					
ORGANISM	1 (sites)					
REFERENCE	cabazon Silva, T.E. and Delisse, A.M.					
AUTHORS	triple fusion proteins comprising ubiquitin fused between					
TITLE	thioredoxin and a polypeptide of interest					
JOURNAL	Patent: WO 0200892-A 1 03-JAN-2002;					
FEATURES	SmithKline Beecham Biologics SA (BE)					
source	Location/Qualifiers					
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	/organism="synthetic construct"					
	/db_xref="taxon:32630"					
	/note="Chimaeric (E. coli - human)"					
BASE COUNT	391 a	400 c	433 g			
ORIGIN						
Query Match 95.0%; Score 213.8; DB 6; Length 1569;						
Best Local Similarity 96.9%; Pred. No. 2.2e-40;						
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;						
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Qy	61	GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCTGGGCGCTC	120			
Db	1090	GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGGCCACTGCTGGGCGCTC	1149			
Qy	121	TCCTACGATGGCCCTGCTGGGTGACAATCAGATCATGCCCCAGGACAGGCTTCTCTGATAATC	180			
Db	1150	TCCTACGATGGCCCTGCTGGGTGACAATCAGATCATGCCCCAGGACAGGCTTCTCTGATAATC	1209			
Qy	181	ATCTGGCCATAATCGCAAGAGAGGGGACGTGTGCCCTGTAGAGG	225			
Db	1210	GTCCTGGCCATAATCGCAAGAGAGGGGACGTGTGCCCTGTAGAGG	1254			
RESULT 13						
LOCUS	AR153502	1640 bp	linear			
DEFINITION	Sequence 11 from patent US 6235525.					
ACCESSION	AR153502					
VERSION	AR153502.1	GI:15121034				
KEYWORDS	unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 1640)					
AUTHORS	van den Eynde, B., van der Bruggen, P. and Boon-Falleur, T.					
TITLE	Isolated nucleic acid molecules coding for tumor rejection antigen					
JOURNAL	precursor Mage-3 and uses thereof					
FEATURES	Patent: US 6235525-A 11 22-MAY-2001;					
	Location/Qualifiers					

LOCUS BC011744 1663 bp mRNA linear PRI 02-AUG-2001
DEFINITION Homo sapiens, similar to melanoma antigen, family A, 3, clone
MGC:19667 IMAGE:3345801, mRNA, complete cds.
ACCESSION BC011744
VERSION BC011744.1 GI:15079897
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1663)
Strausberg R.
Direct Submission
Submitted (30-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.H., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, Q.L., Masiello, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,
Tiongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 27 Row: b Column: 12
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.

FEATURES

Location/Qualifiers
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/db_xref="taxon:9606"
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/lab_host="DH10B-R"
/note="Vector: pOTB7"
145..1089
/codon_start=1
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/protein_id="AAH1744.1"
/db_xref="GI:15079898"
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SEFOALSKVALVHLLKYAREPVTAKMLGSYGVNWQYFFPVIESKASSLQL
VFGILEMVDPTGLHYIFATCLGSLDGLDQNIKPKAGLLIIVLAIAREDCAPE
EKIWELSVLEFVEDRESILGDPKLLTOHFQENYLEYRQVPGSDPACYEFLWGP
ALVETSYKVLHMKVIGSGPHISYPLPHEWVLRGEE"
BASE COUNT 411 a 398 c 448 g 406 t
ORIGIN

Query Match 95.0%; Score 213.8; DB 9; Length 1663;
Best Local Similarity 96.9%; Pred. No. 2.2e-40;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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|||||
DB 577 TATTCTCTTCCTGATCTTCAGCAAGCTCCGATTCCTTCAGCTGGTCTTTGGCATC 636

QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACTGCTGGGCTC 120
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DB 637 GAGCTGATGGAAGTGGACCCCATCGGCCACTTGTACATCTTTGCCACTGCTGGGCTC 696
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QY 121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 180
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DB 697 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 756
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QY 181 ATCCTGGCCCATATATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
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DB 757 GTCCTGGCCCATATATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 801
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Search completed: September 4, 2002, 16:38:28
Job time: 19506 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 4, 2002, 14:29:00 ; Search time 114.14 seconds
(without alignments)
3384.491 Million cell updates/sec

Title: US-08-967-727-18

Perfect score: 225

Sequence: 1 TATTTCCTTCTGTGTGATCTT.....GCGACTGTGCCCTCAGGAG 225

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	225	100.0	225 13	AAQ32362
2	225	100.0	225 15	AAQ72487
3	225	100.0	225 20	AAQ84112
4	223.4	99.3	225 16	AAQ84116
5	220.2	97.9	1362 20	AAQ87596
6	220.2	97.9	1375 19	AAQ22716
7	220.2	97.9	4204 22	AAQ02056
8	213.8	95.0	666 22	AAQ18141
9	213.8	95.0	945 22	AAQ12993

10	213.8	95.0	1212	20	AAQ87592
11	213.8	95.0	1353	20	AAQ87588
12	213.8	95.0	1640	15	AAQ72480
13	213.8	95.0	1640	20	AAQ84116
14	213.8	95.0	4204	20	AAQ26974
15	213.8	95.0	4204	21	AAQ37927
16	213.8	95.0	4204	22	AAQ18140
17	212.2	94.3	1640	13	AAQ32355
18	196.8	87.5	727	22	AAQ21285
19	195.2	86.8	920	22	ABA36364
20	195.2	86.8	920	22	AAQ24300
21	195.2	86.8	920	22	AAQ149576
22	195.2	86.8	1030	22	AAQ1286
23	195.2	86.8	1956	22	ABA26487
24	195.2	86.8	1956	22	AAI15118
25	195.2	86.8	1956	22	AAI36453
26	195.2	86.8	4157	13	AAQ32353
27	195.2	86.8	4157	15	AAQ72478
28	195.2	86.8	4157	20	AAQ84114
29	195.2	86.8	4523	22	AAQ06131
30	166	73.8	379	18	AAQ63345
31	163.2	72.5	930	22	AAQ12987
32	163.2	72.5	1084	15	AAQ67866
33	163.2	72.5	1084	20	AAQ08442
34	163.2	72.5	1094	15	AAQ67865
35	163.2	72.5	1094	20	AAQ08441
36	163.2	72.5	1338	20	AAQ87593
37	163.2	72.5	1341	20	AAQ87591
38	163.2	72.5	1624	22	AAQ24676
39	163.2	72.5	1691	20	AAQ69719
40	163.2	72.5	2418	20	AAQ84103
41	163.2	72.5	2419	13	AAQ32351
42	163.2	72.5	2419	15	AAQ72476
43	163.2	72.5	2419	16	AAQ05086
44	163.2	72.5	2419	20	AAQ84112
45	163.2	72.5	2420	15	AAQ72472

ALIGNMENTS

RESULT 1
AAQ32362
ID AAQ32362 standard; DNA; 225 BP.

AC AAQ32362;

DT 22-APR-1993 (first entry)

DE MAG-6 gene.

OS Melanoma antigen; MAG-6 gene.
PN tumor rejection antigen precursor; MAG-6 gene family; ss.
PD Homo sapiens.

PN WO9220356-A.

PD 26-NOV-1992.

PF 22-MAY-1992; 92WO-US04354.

PR 23-MAY-1991; 91US-0705702.

PR 09-JUL-1991; 91US-0728838.

PR 23-SEP-1991; 91US-0764364.

PR 12-DEC-1991; 91US-0807043.

(LUDW-) LUDWIG INST CANCER RES.

PI Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;

PI Van Den Eynde B, Van Der Bruggen P, Van Pel A;

XX WPI; 1992-415460/50.

DR

XX Nucleic acid mol. encoding a human tumour rejection antigen
PT precursor - useful as an immunostimulant in a vaccine for
PT treating and preventing cancers, also useful in diagnosis
XX
XX Disclosure; Page 88; 142pp; English.
XX
CC The sequences given in AAQ32352-69 represent a new family of genes
CC referred to as melanoma antigens (MAGE). The cDNAs of this gene
CC family were identified during the isolation of the antigen E gene.
CC The MAGE cDNAs, when tested, did not transfer expression of antigen
CC E, but they did show substantial homology to the antigen E cDNA
CC sequence. The MAGE DNAs share a certain degree of homology with each
CC other and are expressed in tumour cells including several types of
CC human tumor cells as well as in human tumors. MAGE expression is not
CC restricted to melanomas. MAGE refers to a family of tumor rejection
CC antigen precursors. The antigens resulting from these genes are
CC referred to as MAGE TRAs or melanoma antigen tumor rejection antigens.
CC See also AAQ32351.

XX Sequence 225 BP; 44 A; 65 C; 58 G; 58 T; 0 other;

Query Match 100.0%; Score 225; DB 13; Length 225;
Best Local Similarity 100.0%; Pred. No. 6.6e-56;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 tattttcttctgtgattcttcagcaaaagcttcgattcttcgtgacgtgtctttggcatc 60
Qy 61 GAGCTGATGGAAGTGGACCCCATCGGACGCTGTACATCTTTGGCACCTGCTGGGCCTC 120
Db 61 gagctgatggaagtggaccccatcgccacgtgtacatctttgccaacctgctgggcctc 120
Qy 121 TCCTACGATGGCCTGCTGGGTGACAAATCAGATCATGCCAGGACAGGCTTCTGTATATC 180
Db 121 tcctacgatggcctgctgggtgacaatcagatcatgcccaggacaggcttctgtataatc 180
Qy 181 ATCTCTGGCCATAATCGCAAGAGGCGGACGTGTGCCCTCGAGGAG 225
Db 181 atctctggccataatcgcaagagggcgactgtgcccctgaggag 225

RESULT 2
AAQ72487
ID AAQ72487 standard; cDNA to mRNA; 225 BP.

XX AC AAX84122;
XX DT 08-SEP-1999 (first entry)
XX DE MAGE-6 gene.
XX KW Tumour rejection antigen MAGE-6 cDNA.
XX DE
XX KW Tumour rejection antigen; melanoma antigen-6; MAGE-6; MAGE-3;
KW cancer; cytolytic T cells; antigen D; human leucocyte antigen;
ss.

XX Homo sapiens.
XX PN W09423031-A.
XX PD 13-OCT-1994.
XX PF 17-MAR-1994; 94WO-US02877.
XX PR 26-MAR-1993; 93US-0037230.
XX PA (LUDW-) LUDWIG INST CANCER RES.

XX Boon-falleur T, Gaugler B, Van DEN EYNDE B, Van DER BRUGGEN P;
XX WPI; 1994-333192/41.
XX

XX New tumour rejection antigen precursor MAGE3 - useful in
PT treatment and diagnosis of cancer
XX
XX Example 32; Page 73; 105pp; English.
XX
CC AAQ72487 is the cDNA sequence which codes for melanoma antigen-6
CC (MAGE-6). Another melanoma antigen MAGE-3 is encoded by
CC AAQ72470, this is a tumour rejection antigen precursor. Melanomas
CC characterised by the expression of MAGE-3 can be detected, or
CC monitored, by contacting a test sample with an agent that can
CC recognise MAGE-3. The melanoma can be treated by the administration
CC of cytolytic T cells specific for the complex of antigen D (the
CC mature rejection antigen derived from MAGE-3) and a human leucocyte
CC antigen (esp. HLA-A1).
XX
XX Sequence 225 BP; 44 A; 65 C; 58 G; 58 T; 0 other;

Query Match 100.0%; Score 225; DB 15; Length 225;
Best Local Similarity 100.0%; Pred. No. 6.6e-56;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATTTCCTTCCTGTGATCTTCAGCAAGCTTCCGATTCCTTGACGTGGTCTTTGGCATC 60
Db 1 tattttcttctgtgattcttcagcaaaagcttcgattcttcgtgacgtgtctttggcatc 60
Qy 61 GAGCTGATGGAAGTGGACCCCATCGGACGCTGTACATCTTTGGCACCTGCTGGGCCTC 120
Db 61 gagctgatggaagtggaccccatcgccacgtgtacatctttgccaacctgctgggcctc 120
Qy 121 TCCTACGATGGCCTGCTGGGTGACAAATCAGATCATGCCAGGACAGGCTTCTGTATATC 180
Db 121 tcctacgatggcctgctgggtgacaatcagatcatgcccaggacaggcttctgtataatc 180
Qy 181 ATCTCTGGCCATAATCGCAAGAGGCGGACGTGTGCCCTCGAGGAG 225
Db 181 atctctggccataatcgcaagagggcgactgtgcccctgaggag 225

RESULT 3
AAX84122
ID AAX84122 standard; cDNA; 225 BP.

XX AC AAX84122;
XX DT 08-SEP-1999 (first entry)
XX DE MAGE-6 gene.
XX KW Tumour rejection antigen; vaccine; cancer; MAGE-6 gene; ss.
XX OS Homo sapiens.
XX PN US5925729-A.
XX PD 20-JUL-1999.
XX PF 02-MAY-1994; 94US-0142368.
XX PR 02-MAY-1994; 94US-0142368.
XX PR 23-MAY-1991; 91US-0705702.
XX PR 09-JUL-1991; 91US-0728838.
XX PR 23-SEP-1991; 91US-0764365.
XX PR 12-DEC-1991; 91US-0807043.
XX PA (LUDW-) LUDWIG INST CANCER RES.

XX Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;
XX Van Den Eynde B, Van Der Bruggen P, Van Pel A;
XX WPI; 1999-418294/35.
XX

PT New tumour rejection antigen is useful as a vaccine against
PT cancerous diseases
XX
PS Disclosure; Column 69-70; 58pp; English.
PS
CC This sequence represents the MAGE-6 gene sequence.
CC The invention relates to a tumour rejection antigen sequence that is
CC useful as a tumour rejection antigen for vaccination against cancerous
CC conditions.
XX
SQ Sequence 225 BP; 44 A; 65 C; 58 G; 58 T; 0 other;

Query Match 100.0%; Score 225; DB 20; Length 225;
Best Local Similarity 100.0%; Pred. No. 6.6e-56;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATTTCCTTCCTGATCTTCAGCAAGCTTCGGATTCCTTCGAGCTGGTCTTTGGCATT 60
DB 1 tatttcttctgtgatcttcagcaagcttcggattcttcgagcttgctcttggcattc 60
QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCGTGGGCCTC 120
DB 61 gagctgatggagtggaagtgacccttcgcccacgtgtacatctttgccacctgcttgggcctc 120
QY 121 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCAGGACAGGCTTCCTGTGATAATC 180
DB 121 tctacgatggcctgctgggtgacaaatcagatcatgccagagagagcttctctgataatc 180
QY 181 ATCCCTGCCATATTCAGCAAGAGGGCGACTGTGCCCTTGAGGAG 225
DB 181 atccctggcataatcgcaagagaggcgactgtgcccttgaggag 225

RESULT 4
ART01166
ID AAT01166 standard; DNA; 225 BP.
XX
AC AAT01166;
XX
DT 26-FEB-1996 (first entry)
DE MAGE-6 gene.
XX
KW MAGE-6; melanoma; tumour rejection antigen; cancer; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9523874-A1.
XX
PD 08-SEP-1995.
XX
PF 23-FEB-1995; 95WO-US02203.
XX
PR 30-NOV-1994; 94US-0346774.
PR 01-MAR-1994; 94US-0204727.
PR 10-MAR-1994; 94US-0209172.
PR 01-SEP-1994; 94US-0299849.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Boon-Falleur T, Brasseur F, Chomez P, De Plaen B;
PI De Smet C, Gaugler B, Lethe B, Marchand M, Patard J;
PI Szikora J, Van Den Eynde B, Van Derbruggen P, Weynants P;
XX
WPI; 1995-320586/41.
DR
XX Determn. of cancerous condition(s) - using a nucleic acid as a
PT primer to determine expression of a MAGE tumour rejection antigen
PT precursor
XX
PS Example 32; Page 80; 121pp; English.
XX

CC A family of human tumour rejection antigen precursor, MAGE, genes
CC (AAT05091-99, AAT01165-71) was isolated from various tumour cell lines.
CC cDNA (AAT01166) coding for MAGE-6 was obtd. from human melanoma
CC LB-33-MEL cells. MAGE serve as markers for tumour diagnosis. The
CC genes are silent in normal cells.
XX
SQ Sequence 225 BP; 44 A; 66 C; 57 G; 58 T; 0 other;

Query Match 99.3%; Score 223.4; DB 16; Length 225;
Best Local Similarity 99.6%; Pred. No. 1.9e-55;
Matches 224; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TATTTCCTTCCTGATCTTCAGCAAGCTTCGGATTCCTTCGAGCTGGTCTTTGGCATT 60
DB 1 tatttcttctgtgatcttcagcaagcttcggattcttcgagcttgctcttggcattc 60
QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCGTGGGCCTC 120
DB 61 gagctgatggagtggaagtgacccttcgcccacgtgtacatctttgccacctgcttgggcctc 120
QY 121 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCAGGACAGGCTTCCTGTGATAATC 180
DB 121 tctacgatggcctgctgggtgacaaatcagatcatgccagagagagcttctctgataatc 180
QY 181 ATCCCTGCCATATTCAGCAAGAGGGCGACTGTGCCCTTGAGGAG 225
DB 181 atccctggcataatcgcaagagaggcgactgtgcccttgaggag 225

RESULT 5
AAX87596
ID AAX87596 standard; cDNA; 1362 BP.
XX
AC AAX87596;
XX
DT 26-OCT-1999 (first entry)
XX
DE CLYTA-MAGE-3-His fusion DNA.
XX
KW MAGE-3; CLYTA-MAGE-3-His; fusion protein; tumour; melanoma;
KW breast cancer; bladder cancer; lung cancer; colon cancer;
KW head and squamous cell carcinoma; oesophagus carcinoma; vaccine;
KW human; ss.
XX
OS Chimeric - Streptococcus pneumoniae.
OS Chimeric - Homo sapiens.
OS Chimeric - synthetic.
XX
PN WO9940188-A2.
XX
PD 12-AUG-1999.
XX
PF 02-FEB-1999; 99WO-EP00660.
XX
PR 06-FEB-1998; 98GB-0002650.
PR 05-FEB-1998; 98GB-0002543.
XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Cabezon Silva T, Cohen J, Slaoui MM, Vinals Bassols C;
XX
DR WPI; 1999-494293/41.
DR P-PSDB; AAY06593.
XX
PT New protein derivatives used in cancer vaccine therapy for treating
PT a range of cancers including melanomas, carcinomas and cancers of
PT breast
XX
PS Example 10; Page 72; 72pp; English.
XX
CC This DNA sequence codes for a fusion protein (see AAY06593) composed
CC of the C-terminal portion of the Streptococcus pneumoniae LYTA

CC protein (CLYTA), the human MAGE-3 tumour-associated antigen and a
CC hexahistidine tail. A vector designed for recombinant expression
CC of the fusion protein in *Escherichia coli* is provided. The CLYTA
CC moiety provides expression of soluble fusion protein, facilitates
CC affinity purification of the fusion protein, and also acts as a
CC T-helper epitope. The invention relates to MAGE proteins fused to
CC an immunological fusion partner, e.g. CLYTA-MAGE-3-His. These novel
CC fusion proteins provide vaccines for immunotherapy of melanomas or
CC other MAGE-associated tumours like breast, bladder, lung and
CC non-small cell lung cancer, head and squamous cell carcinoma, colon
CC carcinoma and oesophagus carcinoma.
XX
SQ Sequence 1362 BP; 345 A; 348 C; 383 G; 286 T; 0 other;

Query Match 97.9%; Score 220.2; DB 20; Length 1362;
Best Local Similarity 98.7%; Pred. No. 2.8e-54;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTGACGCTGGTCTTTGGGCATC 60
DB 823 tactttctctgtgtcttcagcaagcttcgattccttcagctggcttttggcattc 882
QY 61 GAGCTGATGGAGTGGACCCCATCGGCACGCTGACATCTTGGCCACCTGCTGGGCTC 120
DB 883 gagctgatggaagtggacccttcgccaagctgtacatcttggccactgctgggctc 942
QY 121 TCCTACGATGGCTGCTGGTGACAATCAGATCATGCCCCAGCAGGCTTCTGTATATC 180
DB 943 tcttaagatggctgctgggtgacaatcagatcatgccaagacaggtcttctgataatc 1002
QY 181 ATCTGCGCCATAATCGCAAGAGAGGGCGACTGTGCCCTTGAGGAG 225
DB 1003 atcttgccataatcgcaaaaggcgactgtgcccttgaggag 1047

RESULT 6
AAV22716
ID AAV22716 standard; DNA; 1375 BP.
XX
AC AAV22716;
XX
DT 18-AUG-1998 (first entry)
XX
DE MAGE-6 cDNA.
XX
KW Human tumor rejection antigen precursor; TRA; MAGE-6; HLA-Cw*16;
KW major histocompatibility complex; MHC; cytotoxic T-cell; ss.
XX
OS Homo sapiens.
XX
PN WO9810780-A1.
XX
PD 19-MAR-1998.
XX
PF 27-AUG-1997; 97WO-US15069.
XX
PR 13-SEP-1996; 96US-0713354.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Boon-Falleur T, DePlaen E, Van Der Bruggen P;
XX
DR WPI; 1998-207144/18.
XX
PT Tumour rejection antigen precursor, MAGE-6 derived peptide(s) which
PT bind to HLA-Cw*16 - used for provoking proliferation of cytotoxic T
PT cells, useful for, e.g. treatment of cancerous cells
XX
PS Disclosure; Page 19; 31pp; English.
XX
CC The present sequence represents a MAGE-6 cDNA encoding a human tumor
CC rejection antigen (TRA) precursor. The invention provides for TRAs

CC (AAW56268-W56272) which are processed from TRA precursors that are
CC derived from the MAGE-6 gene. The TRAs bind to major histocompatibility
CC complex (MHC) molecules of the type HLA-Cw*16 to provoke a cytotoxic
CC T-cell response against cells exhibiting this particular TRA-MHC
CC complex. As the cells presenting these complexes are human cancerous
CC cells, the TRA peptides are claimed to be useful in provoking lysis of
CC these cancerous cells thereby providing a probable method of treating
CC cancer.
XX
SQ Sequence 1375 BP; 293 A; 364 C; 404 G; 314 T; 0 other;

Query Match 97.9%; Score 220.2; DB 19; Length 1375;
Best Local Similarity 98.7%; Pred. No. 2.8e-54;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTGACGCTGGTCTTTGGGCATC 60
DB 592 tactttctctgtgtcttcagcaagcttcgattccttcagctggcttttggcattc 651
QY 61 GAGCTGATGGAGTGGACCCCATCGGCACGCTGTACATCTTGGCCACCTGCTGGGCTC 120
DB 652 gagctgatggaagtggacccttcgccaagctgtacatcttggccactgctgggctc 711
QY 121 TCCTACGATGGCTGCTGGTGACAATCAGATCATGCCCCAGCAGGCTTCTGTATATC 180
DB 712 tcttaagatggctgctgggtgacaatcagatcatgccaagacaggtcttctgataatc 771
QY 181 ATCTGCGCCATAATCGCAAGAGAGGGCGACTGTGCCCTTGAGGAG 225
DB 772 atcttgccataatcgcaaaaggcgactgtgcccttgaggag 816

RESULT 7
AAS02056
ID AAS02056 standard; cDNA; 4204 BP.
XX
AC AAS02056;
XX
DT 16-JUL-2001 (first entry)
XX
DE DNA encoding molecule for disease detection and treatment, mddt21.
XX
KW Human; mddt21; gene therapy; adenosine deaminase deficiency;
KW ADA; severe combined immunodeficiency syndrome; cystic fibrosis;
KW thalassemia; familial hypercholesterolemia; haemophilia; factor VIII;
KW factor IX; cancer; cell proliferation; parasite; human retrovirus; HIV;
KW hepatitis B; hepatitis C; Candida albicans; Plasmodium falciparum;
KW Paracoccidioides brasiliensis; Trypanosoma brasiliensis; ss.
XX
OS Homo sapiens.
XX
PN WO200123538-A2.
XX
PD 05-APR-2001.
XX
PF 22-SEP-2000; 2000WO-US26085.
XX
PR 28-SEP-1999; 99US-0156565.
XX
PR 30-NOV-1999; 99US-0168197.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Hodgson DM, Lincoln SE, Russo FD, Spiro PA, Banville SC;
PI Bratcher SR, Dufour GE, Cohen HJ, Rosen BH, Shah P, Chalup MS;
PI Hillman JL, Jones AL, Yu JY, Greenawalt LB, Panzer SR;
PI Roseberry AM, Wright RJ, Chen W, Liu TF, Yap PE, Stockdreher TK;
PI Anshey S, Fong WT;
XX
DR WPI; 2001-258131/26.
XX
PT Purified disease treatment and detection molecule polynucleotides and
PT polypeptides, useful for providing diagnostic assays and gene therapy

[illegible]

Claim 1; Page 109-110; 113pp; English.

The sequence represents the coding sequence of molecule for disease detection and treatment, mddt21, shown by computer analysis to be similar to the MAGE family of proteins. The sequence may be used for somatic or germline gene therapy. Gene therapy may be performed to: (i) correct genetic deficiency such as in severe combined immunodeficiency syndrome associated with adenosine deaminase (ADA) deficiency, cystic fibrosis, thalassemias, familial hypercholesterolemia and haemophilia caused by factor VIII or factor IX deficiencies; (ii) express a conditional lethal gene product (such as in the case of cancers which result from unregulated cell proliferation); (iii) express a protein which affords protection against intracellular parasites (for example, human retroviruses such as HIV, hepatitis B or C, fungal parasites such as Candida albicans and Paracoccidioides brasiliensis, and protozoal parasites such as Plasmodium falciparum and Trypanosoma brasiliensis.

Sequence 4204 BP; 947 A; 1145 C; 1219 G; 893 T; 0 other;

Query Match	97.9%;	Score 220.2;	DB 22;	Length 4204;
Hit Local Similarity	98.7%;	Pred. No. 3.9e-54;		
Matches 222;	Conservative	0;	Mismatches 3;	Indels 0;
Gaps	0;			
1	TATTTCCTTCCTGATCTTCAGCAAGCTTCGCCGATTCCTTGCAGCTGGCTTTGGCATC	60		
2897	tacttcttctgtatcttcgaaagcttcgattccttgagctggctcttggcattc	2956		
61	GAGCTGATGGAGTGGACGCCCATCGGCCACGTTGACATCTTTGGCCACTGCCCTGGGGCCTC	120		
2957	gagctgtggaagtggagcccatcgccacgtgtacattcttggccactgctggggcctc	3016		
121	TCCTACCATGCGCTGCTGGTGACATCATGATGCCAGAGCAGAGCTTCCTCGATAATC	180		
3017	tcctacgatggctcgtcgtgggtgacaatcagatccatgccaagacaggtctcctcgataatc	3076		
181	ATCTCGGCCATAATCGCAAGAGAGGGCGGCACTGTGCCCTGAGGAG	225		
3077	atctcgccataatcgcaaaagaggcgactgtgccctgaggag	3121		

T 8
1141
AAD18141 standard; cDNA; 666 BP.
AAD18141;
18-DEC-2001 (first entry)
Human melanoma associated antigen 3 (MAGE-3) truncated cDNA.
Human; melanoma associated antigen 3; MAGE-3; neuroprotective; neurotropic; immunosuppressive; caspase-12 activation; cell death related disease; cell death inhibitor; cancer-specific protein; Alzheimer's disease; neurodegenerative disease; autoimmune disease; anyotrophy; gene therapy; organ disorder; ss.
Homo sapiens.
Key Location/Qualifiers
CDS 1..666
/tag= a
/product= "Human MAGE-3 protein"
/note= "CDS does not include start codon"
/partial
EP1126027-A1.
22-AUG-2001.
16-FEB-2001; 2001EP-0301361.

PR	18-FEB-2000; 2000JP-0041927.
XX	(RIKE) RIKEN KK.
PA	Morishima N, Shibata T;
PI	
XX	WPI: 2001-591501/67.
DR	P-PSDB; AAE10673.
XX	
XX	New polypeptide for treating cell death related diseases such as
PT	Alzheimer's disease, neurodegenerative diseases, autoimmune diseases
PT	amyotrophy and organ disorders comprises the recombinant
PT	cancer-specific protein MAGE-3 -
XX	
PS	Claim 3; Page 25-27; 41pp; English.
XX	
CC	The present sequence is the truncated form of human melanoma
CC	associated antigen 3 (MAGE-3) cDNA. The present invention relates
CC	to MAGE-3 protein or its truncated form which specifically bind to
CC	caspase-12 or pro-caspase-12 protein and inhibit their activation.
CC	MAGE-3 proteins are cancer-specific proteins and are used as cell-
CC	death inhibitors. Therapeutic agents comprising MAGE-3 sequence are
CC	useful for treating cell death related diseases such as Alzheimer s
CC	disease, neurodegenerative diseases, autoimmune diseases, amyotrophy
CC	and organ disorders. MAGE-3 gene is useful as an agent for gene therapy
CC	The sequences of the invention are useful for preventing or treating
CC	cell death-related disease developing in tissues in the nervous system,
CC	vascular system, respiratory system, digestive system, lymph system,
CC	urinary system, or reproductive system.
XX	
SQ	Sequence 666 BP; 151 A; 165 C; 197 G; 153 T; 0 other;
Query Match	95.0%; Score 213.8; DB 22; Length 666;
Best local Similarity	96.9%; Pred. No. 1.6e-52;
Matches 218; Conservative	0; Mismatches 7; Indels 0; Gaps
QY	1 TATTTCCTTCTCGTGATCTTCAGCAAAAGCTTCCGATTCTTCGTGCAGCTGGTCTTTGGCATC 60
Db	154 tattttcttcgtgatcttccagcaaaagtctcgaagtgcgcttggtctttggcatc 213
QY	61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120
Db	214 gagctgatggaagtggaccocatcgccacttgtacatctttgccacctgctggcgctc 273
QY	121 TCCTACCATGGCCTGCTGGGTGACAATCAGATCATGCCACAGGACAGGCTTCCTGATTAATC 180
Db	274 tcctcacgatgctgctggtgacaatcagatcatgcccaaggcaggcctcctgataac 333
QY	181 ATCTCTGGCCATAATCGCAAGAGGGGACTGTGCCCTTGAGGAG 225
Db	334 gtcttgccataatcgcgaagagaggcgactgtgcccttgaggag 378
RESULT	9
AAD12993	
ID	AAD12993 standard; DNA; 945 BP.
XX	
AC	AAD12993;
XX	
DT	16-OCT-2001 (first entry)
XX	
DE	Human MAGE-A3 DNA.
XX	
KW	MAGE antigenic peptide; Human leukocyte antigen; HLA-B35; HLA-B44;
KW	tumour cell; immunostimulant; antigen presentation; cancer; melanoma;
KW	Cd8+ cytotoxic T lymphocyte; colorectal; prostate; gastric carcinoma;
KW	myeloma; brain tumour; sarcoma; seminoma; ovarian tumour; cytotstatic;
KW	gene therapy; human; MAGE-A3; tumour rejection antigen; TRA; ds.
XX	
OS	Homo sapiens.
PH	
Key	Location/Qualifiers

```

FT CDS      1..945
FT          /*tag= a
FT          /product= "MAGE-A3 protein"
XX
XX PN       WO200153833-A1.
XX
XX PD       26-JUL-2001.
XX
XX PF       19-JAN-2001; 2001WO-US02008.
XX
XX PR       20-JAN-2000; 2000US-0177242.
XX
XX PR       25-OCT-2000; 2000US-0243212.
XX
XX PA       (LUDW-) LUDWIG INST CANCER RES.
XX
XX PI       Luiten R, Boon-Falleur T, Van Der Bruggen P, Stroobant V;
XX
XX PI       Demotte N, Schultz E;
XX
XX DR       WPI; 2001-488724/53.
XX
XX DR       P-PSDB; AAE06853.
XX
XX PT       Functional variants and isolated mimetics of a MAGE-A1 HLA-B35 or
XX
XX PT       HLA-B44 binding peptide, or of a MAGE-A3 HLA-B35 binding peptide, used
XX
XX PT       in diagnosis and treatment of a disorder characterized by expression of
XX
XX PT       MAGE-A1 or -A3.
XX
XX PS       Example 3; Page 94-95; 103pp; English.
XX
XX CC       The invention relates to functional variants and isolated mimetics of a
XX
XX CC       MAGE-A1 human leukocyte antigen (HLA)-B35 or HLA-B44 binding peptide,
XX
XX CC       or of a MAGE-A3 HLA-B35 binding peptide, identified by methods described
XX
XX CC       in the specification. MAGE genes encode tumour rejection antigens
XX
XX CC       (TRAS) presented to T lymphocytes by HLA-B35 and HLA-B44 molecules.
XX
XX CC       The MAGE antigenic peptide acts by binding to HLA molecules
XX
XX CC       on tumour cells and stimulating recognition of these cells and thus
XX
XX CC       signalling them to the immune system for destruction. The peptide when
XX
XX CC       presented by HLA molecule induces the activation and stimulation of
XX
XX CC       CD8+ cytotoxic T lymphocytes. The MAGE antigenic peptide is used to
XX
XX CC       treat and diagnose disorders characterised by expression of MAGE-A1
XX
XX CC       or -A3. Disorders include cancers e.g melanomas, oesophageal, lung,
XX
XX CC       head and neck, breast, colorectal, prostate, renal, bladder,
XX
XX CC       hepatocellular, papillary thyroid and gastric carcinomas, myelomas,
XX
XX CC       brain tumours, sarcomas, seminomas, and ovarian tumours. The present
XX
XX CC       sequence is human MAGE-A3 DNA.
XX
XX SQ       Sequence 945 BP; 210 A; 254 C; 278 G; 203 T; 0 other;

Query Match      95.0%; Score 213.8; DB 22; Length 945;
Best Local Similarity 96.9%; Pred. No. 1.8e-52;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTTCCTTCCTGATCTTCAGCAAGCTTCAGATTCCTTCAGCTGCTTTGGCATC 60
   |||||||
DB 433 tattttcttcctgctgcttcagcaagcttcagttcttcctgagctgtgtcttggcatc 492
   |||||||

QY 61 GAGCTGATGGAAGTGGACCCCATCGCCACGTGTACATTTTGCACCTGCTGGGCCCTC 120
   |||||||
DB 493 gagctgatggaagtggaccccatcgccacttgatcatcttggcactgctgggacctc 552
   |||||||

QY 121 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCACGACAGGCTTCTGTATATC 180
   |||||||
DB 553 tctctacgatggctgctgggtgacaaatcagatcatgcccaaggcgctctcgtataatc 612
   |||||||

QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTTGAGGAG 225
   |||||||
DB 613 gtccctggccataatcgcaagagagggcgactgtgcccttgaggag 657
   |||||||

RESULT 10
AA87592
ID AAX87592 standard; cDNA; 1212 BP.
XX

```

```

AC AAX87592;
XX
XX DT       26-OCT-1999 (first entry)
XX
XX DE       Haemagglutinin-MAGE-3-His fusion DNA.
XX
XX KW       MAGE-3; haemagglutinin; NSI-MAGE-3-His; fusion protein; tumour;
XX
XX KW       melanoma; breast cancer; bladder cancer; lung cancer;
XX
XX KW       head and squamous cell carcinoma; colon cancer;
XX
XX KW       oesophagus carcinoma; vaccine; human; ss.
XX
XX OS       Chimeric - Influenza virus.
XX
XX OS       Chimeric - Homo sapiens.
XX
XX OS       Chimeric - synthetic.
XX
XX PN       WO9940188-A2.
XX
XX PD       12-AUG-1999.
XX
XX PF       02-FEB-1999; 99WO-EP00660.
XX
XX PR       06-FEB-1998; 98GB-0002650.
XX
XX PR       05-FEB-1998; 98GB-0002543.
XX
XX PA       (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX PI       Cabezon Silva T, Cohen J, Slaoui MM, Vinals Bassols C;
XX
XX DR       WPI; 1999-494293/41.
XX
XX DR       P-PSDB; AAY06591.
XX
XX PT       New protein derivatives used in cancer vaccine therapy for treating
XX
XX PT       a range of cancers including melanomas, carcinomas and cancers of
XX
XX PT       breast
XX
XX PS       Example 7; Page 69; 72pp; English.
XX
XX CC       This DNA sequence codes for a fusion protein (see AAY06591) composed
XX
XX CC       of haemagglutinin NSI of influenza virus, the human MAGE-3
XX
XX CC       tumour-associated antigen and a hexahistidine tail. A vector
XX
XX CC       designed for recombinant expression of the fusion protein is
XX
XX CC       provided. MAGE-3 cDNA was amplified using primers that altered the
XX
XX CC       first 5 codons to Escherichia coli codon usage. The NSI moiety
XX
XX CC       provided the fusion protein with additional exogenous T-helper
XX
XX CC       epitopes. The invention relates to MAGE proteins fused to an
XX
XX CC       immunological fusion partner, e.g. NSI-MAGE-3-His. These novel
XX
XX CC       fusion proteins provide vaccines for immunotherapy of melanomas or
XX
XX CC       other MAGE-associated tumours like breast, bladder, lung and
XX
XX CC       non-small cell lung cancer, head and squamous cell carcinoma, colon
XX
XX CC       carcinoma and oesophagus carcinoma.
XX
XX SQ       Sequence 1212 BP; 289 A; 319 C; 344 G; 260 T; 0 other;

Query Match      95.0%; Score 213.8; DB 20; Length 1212;
Best Local Similarity 96.9%; Pred. No. 2e-52;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTTCCTTCCTGATCTTCAGCAAGCTTCAGATTCCTTCAGCTGCTTTGGCATC 60
   |||||||
DB 673 tattttcttcctgctgcttcagcaagcttcagttcttcctgagctgtgtcttggcatc 732
   |||||||

QY 61 GAGCTGATGGAAGTGGACCCCATCGCCACGTGTACATTTTGGCACCTGCTGGGCCCTC 120
   |||||||
DB 733 gagctgatggaagtggaccccatcgccacttgatcatcttggcactgctgggacctc 792
   |||||||

QY 121 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCACGACAGGCTTCTGTATATC 180
   |||||||
DB 793 tctctacgatggctgctgggtgacaaatcagatcatgcccaaggcgctctcgtataatc 852
   |||||||

QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTTGAGGAG 225
   |||||||
DB 853 gtccctggccataatcgcaagagagggcgactgtgcccttgaggag 897
   |||||||

```

```
RESULT 11
AAx87588
ID AAX87588 standard; cDNA; 1353 BP.
XX
XX
AC AAX87588;
XX
XX 26-OCT-1999 (first entry)
XX
XX Lipoprotein D-MAGE-3-His fusion DNA.
XX
XX MAGE-3; lipoprotein D; LPD-MAGE-3-His; fusion protein; tumour;
XX melanoma; breast cancer; bladder cancer; lung cancer;
XX head and squamous cell carcinoma; colon cancer;
XX oesophagus carcinoma; vaccine; human; ss.
XX
OS Chimeric - Haemophilus influenzae.
OS Chimeric - Homo sapiens.
OS Chimeric - synthetic.
XX
XX WO9940188-A2.
XX
XX 12-AUG-1999.
XX
XX 02-FEB-1999; 99WO-EP00660.
XX
XX 06-FEB-1998; 98GB-0002650.
XX
XX 05-FEB-1998; 98GB-0002543.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Cabezón Silva T, Cohen J, Slaoui MM, Vinals Bassols C;
XX
XX WPI: 1999-494293/41.
XX
XX P-PSDB; AAT06589.
XX
XX New protein derivatives used in cancer vaccine therapy for treating
XX a range of cancers including melanomas, carcinomas and cancers of
XX breast
XX
XX Example 1; Page 66; 72pp; English.
XX
XX This DNA sequence codes for a fusion protein (see AAY06589) composed
XX of lipidated protein D (LPD) of Haemophilus influenzae B, the human
XX MAGE-3 tumour-associated antigen and a hexahistidine tail. A
XX vector designed for recombinant expression of the fusion protein is
XX provided. MAGE-3 cDNA was amplified using primers that altered the
XX first 5 codons to Escherichia coli codon usage. The LPD moiety
XX provided the fusion protein with additional exogenous T-cell
XX epitopes and also increased expression levels in E. coli. The
XX lipid tail ensured optimal presentation of the antigen to
XX antigen-presenting cells. The affinity tag facilitated
XX purification. The invention relates to MAGE proteins fused to an
XX immunological fusion partner, e.g. LPD-MAGE-3-His. These novel
XX fusion proteins provide vaccines for immunotherapy of melanomas or
XX other MAGE-associated tumours like breast, bladder, lung and
XX non-small cell lung cancer, head and squamous cell carcinoma, colon
XX carcinoma and oesophagus carcinoma.
XX
XX Sequence 1353 BP; 342 A; 337 C; 354 G; 320 T; 0 other;

Query Match 95.0%; Score 213.8; DB 20; Length 1353;
Best Local Similarity 96.9%; Pred. No. 2e-52;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTCTTCTCTGATCTTCAGCAAGCTTCGGATTCTCTTCAGCTGGTCTTTGGCATC 60
DB 814 TATTCTTCTCTGATCTTCAGCAAGCTTCGGATTCTCTTCAGCTGGTCTTTGGCATC 60
QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGGTGTACATCTTTGCCACCTGCGCGGCCCTC 120
DB 664 GAGCTGATGGAAGTGGACCCCATCGGCCACGGTGTACATCTTTGCCACCTGCGCGGCCCTC 120

us-08-967-727-18.rng
874 gagctgatggaagtggaccccatcgccacttgatcatatttgccacctgctgggcctc 933
121 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCAGGACAGGCTTCCCTGATAATC 180
934 tcctacgatggcctgctgggtgacaatcagatcatgcccaaggcaggcctcctcgataatc 993
181 ATCTCTGGCCATAATCCAAAGAGAGGGCGACTGTGTGCCCTCGAGGAG 225
994 gtcctggccataatcgcaagagagggcgactgtgcccctgaggag 1038

RESULT 12
AAQ72480
ID AAQ72480 standard; cDNA to mRNA; 1640 BP.
XX
XX AC AAQ72480;
XX
XX 22-JUN-1995 (first entry)
XX
XX Tumour rejection antigen precursor MAGE-3 cDNA.
XX
XX Tumour antigen rejection precursor; melanoma antigen-3; MAGE-3;
XX cancer; cytolytic T cells; antigen D; human leucocyte antigen;
XX P1A gene; ss.
XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 172..1116
XX FT /*tag= a
XX
XX WO9423031-A.
XX
XX 13-OCT-1994.
XX
XX 17-MAR-1994; 94WO-US02877.
XX
XX 26-MAR-1993; 93US-0037230.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Boon-falleur T, Gaugler B, Van DEN EYNDE B, Van DER BRUGGEN P;
XX
XX WPI: 1994-333192/41.
XX
XX New tumour rejection antigen precursor MAGE3 - useful in
XX treatment and diagnosis of cancer
XX
XX Example 32; Page 64; 105pp; English.
XX
XX AAQ72480 is the P1A gene fragment which contains the cDNA coding
XX sequence AAQ72470, which encodes melanoma antigen-3 (MAGE-3), a tumour
XX rejection antigen precursor. Melanomas characterised by the expression of
XX MAGE-3 can be detected, or monitored, by contacting a test sample with
XX an agent that can recognise MAGE-3. The melanoma can be treated by the
XX administration of cytolytic T cells specific for the complex of
XX antigen D (the mature rejection antigen derived from MAGE-3) and a
XX human leucocyte antigen (esp. HLA-A1).
XX
XX Sequence 1640 BP; 380 A; 402 C; 457 G; 401 T; 0 other;

Query Match 95.0%; Score 213.8; DB 15; Length 1640;
Best Local Similarity 96.9%; Pred. No. 2.1e-52;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTCTTCTCTGATCTTCAGCAAGCTTCGGATTCTCTTCAGCTGGTCTTTGGCATC 60
DB 604 TATTCTTCTCTGATCTTCAGCAAGCTTCGGATTCTCTTCAGCTGGTCTTTGGCATC 663
QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGGTGTACATCTTTGCCACCTGCGCGGCCCTC 120
DB 664 GAGCTGATGGAAGTGGACCCCATCGGCCACGGTGTACATCTTTGCCACCTGCGCGGCCCTC 723
```


QY 121 TCCTACGATGGCTGTGGTGACATCAGATCATGCCCCAGGACAGGCTTCCTGATAATC 180
|||||
Db 3017 tctacgatgctgctgggtgacaatcagatcatgccccagcaggcctcctgataatc 3076
|||||
QY 181 ATCCTGCCCCAATAATCGAACAGAGGGGAGCTGTGCCCTGAGGAG 225
|||||
Db 3077 gtccctggccaataatcgcaagagaggcgactgtgccctgagagag 3121
|||||
RESULT 15
AAA37927
ID AAA37927 standard; cDNA; 4204 BP.
XX
AC AAA37927;
XX
DT 18-AUG-2000 (first entry)
XX
DE Human MAGE-A3 nucleotide sequence.
XX
KW MAGE-A3; HLA class II; human leukocyte antigen; antibody; vaccine;
KW cancer; human; tumour; tumour associated gene product; ss.
XX
OS Homo sapiens.
XX
PN WO200020581-A1.
XX
PD 13-APR-2000.
XX
PF 15-SEP-1999; 99WO-US21230.
XX
PR 05-OCT-1998; 98US-0166448.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (UYVR-) UNIV VRIJE BRUSSEL.
XX
PI Chaux P, Stroobant V, Boon-Falleur T, Van Der Bruggen P;
PI Schultz ES, Van Snick J, Lethe B, Thielemans K, Corthals J;
PI Heirman C;
XX
DR WPI; 2000-317713/27.
DR P-PSDB; AAB02565.
XX
PT New MAGE-A3 class II binding peptides, useful to diagnose and treat
PT tumours, are fragments of MAGE-A3 which bind to and are presented to T
PT lymphocytes by human leukocyte antigen class II molecules -
XX
PS Example 6; Page 96-98; 119pp; English.
XX
CC The present invention relates to MAGE-A3 (tumour associated gene
CC product) human leukocyte antigen (HLA) class II-binding peptides (see
CC AAB02566-B02595, and AAB02633-B02637). These peptides are presented to T
CC cells in the context of HLA class II molecules. The peptides stimulate
CC the activity and proliferation of CD4+ T lymphocytes. The invention also
CC includes nucleotide sequences encoding MAGE-3A peptides (see AAA37928
CC and AAA37938-A37940). The peptides and nucleotide sequences can be used
CC to create antibodies against the MAGE-A3 peptides, the antibodies,
CC peptides and nucleotide sequences can be used to create a vaccine. The
CC expression of MAGE-3, particularly cancer. The methods can also be used
CC in the diagnosis of disorders associated with MAGE-3 expression. Included
CC in the invention are other human tumour antigens (see AAB02596-B02637),
CC and PCR primers used in the course of the invention (see AAA37929-A37937
CC and AAA37941-A37942).
XX
SQ Sequence 4204 BP; 944 A; 1144 C; 1223 G; 893 T; 0 other;

Query Match 95.0%; Score 213.8; DB 21; Length 4204;
Best Local Similarity 96.9%; Pred. No. 2.8e-52;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 TATTTCCTTCCTGATCTTCAGCAAGCTTCGGATTCCTTCGACGTGGTCTTTGGCATC 60
|||||

Db 2897 tattttcttctgtgatctttcagcaaaagcttccagttccttgcagctgggtctttggcgc 2956
QY 61 GAGCTGATGAAGTGGACCCCATCGCCAGTGTACATCTTGGCCACCTGCCTGGGCTC 120
|||||
Db 2957 gagctgatggaaagtggaccatcgccactgtacatcttggccacctgctggggctc 3016
|||||
QY 121 TCCTACGATGGCTGTGGTGACATCAGATCATGCCCCAGGACAGGCTTCCTGATAATC 180
|||||
Db 3017 tctacgatgctgctgggtgacaatcagatcatgccccagcaggcctcctgataatc 3076
|||||
QY 181 ATCCTGCCCCAATAATCGAACAGAGGGGAGCTGTGCCCTGAGGAG 225
|||||
Db 3077 gtccctggccaataatcgcaagagaggcgactgtgccctgagagag 3121
|||||
Search completed: September 4, 2002, 20:16:17
Job time: 20837 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 4, 2002, 15:38:10 ; Search time 62.69 seconds
(without alignments)
881.601 Million cell updates/sec

Title: US-08-967-727-18

Perfect score: 225

Sequence: 1 TATTTCCTTCCTGATCTT.....CGGACTGTGCCCTGAGGAG 225

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	225	100.0	225	1	US-07-807-043B-15
2	225	100.0	225	1	US-08-299-849B-18
3	225	100.0	225	1	US-08-142-368A-18
4	225	100.0	225	3	US-08-967-727-18
5	225	100.0	225	4	US-08-037-230D-18
6	220.2	97.9	945	4	US-09-056-105-7
7	220.2	97.9	1019	4	US-09-056-105-13
8	220.2	97.9	1375	2	US-08-993-738A-2
9	220.2	97.9	1375	4	US-08-713-354C-2
10	213.8	95.0	1640	1	US-07-807-043B-11
11	213.8	95.0	1640	1	US-08-299-849B-11
12	213.8	95.0	1640	1	US-08-142-368A-11
13	213.8	95.0	1640	3	US-08-967-727-11
14	213.8	95.0	1640	4	US-08-037-230D-11
15	213.8	95.0	4204	2	US-08-928-615-1
16	213.8	95.0	4204	4	US-09-056-105-6
17	213.8	95.0	4204	4	US-09-166-448-1
18	195.2	86.8	4157	1	US-07-807-043B-9
19	195.2	86.8	4157	1	US-08-299-849B-9
20	195.2	86.8	4157	2	US-08-142-368A-9
21	195.2	86.8	4157	3	US-08-967-727-9
22	195.2	86.8	4157	4	US-08-037-230D-9
23	195.2	86.8	4559	4	US-09-056-105-5
24	163.2	72.5	1084	2	US-08-184-009-110
25	163.2	72.5	1084	2	US-08-458-356-110
26	163.2	72.5	1084	4	US-08-460-736-110
27	163.2	72.5	1094	2	US-08-184-009-109

28	163.2	72.5	1094	2	US-08-458-356-109	Sequence 109, App
29	163.2	72.5	1094	4	US-08-460-736-109	Sequence 109, App
30	163.2	72.5	1691	2	US-08-993-118-8	Sequence 8, Appli
31	163.2	72.5	1691	3	US-08-845-528C-8	Sequence 8, Appli
32	163.2	72.5	2419	1	US-07-807-043B-7	Sequence 7, Appli
33	163.2	72.5	2419	1	US-08-299-849B-7	Sequence 7, Appli
34	163.2	72.5	2419	2	US-08-142-368A-7	Sequence 7, Appli
35	163.2	72.5	2419	3	US-08-967-727-7	Sequence 7, Appli
36	163.2	72.5	2419	4	US-08-037-230D-7	Sequence 7, Appli
37	163.2	72.5	2420	1	US-08-465-167A-23	Sequence 23, Appli
38	163.2	72.5	2420	4	US-09-056-105-4	Sequence 4, Appli
39	163.2	72.5	5674	1	US-07-807-043B-8	Sequence 8, Appli
40	163.2	72.5	5674	1	US-08-190-411A-1	Sequence 1, Appli
41	163.2	72.5	5674	1	US-08-299-849B-8	Sequence 8, Appli
42	163.2	72.5	5674	2	US-08-560-024-1	Sequence 1, Appli
43	163.2	72.5	5674	2	US-08-142-368A-8	Sequence 8, Appli
44	163.2	72.5	5674	3	US-08-967-727-8	Sequence 8, Appli
45	163.2	72.5	5674	4	US-08-037-230D-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-07-807-043B-15
; Sequence 15, Application US/07807043B
; Patent No. 5342774
; GENERAL INFORMATION:
; APPLICANT: Boon, Thierry, Van den Eynde, Beno t
; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/807,043B
; FILING DATE: 19911212
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-May-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5342774man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 253.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: singular
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: MAGE-6 gene
; US-07-807-043B-15

APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5925729man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5253.4-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: MAGE-6 gene
US-08-142-368A-18

Query Match 100.0%; Score 225; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.4e-62;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATTCTTCTCTGATCTTCAGCAAGCTTCGGATTCCCTTGACAGCTGGTCTTTGGCATC 60
DB 1 TATTCTTCTCTGATCTTCAGCAAGCTTCGGATTCCCTTGACAGCTGGTCTTTGGCATC 60
QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCTGGGCTC 120
DB 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCTGGGCTC 120
QY 121 TCCTACCATGCGCTGCTGGGTGACAAATCAGATCATGCCAGGACAGCTTCCTGATAATC 180
DB 121 TCCTACCATGCGCTGCTGGGTGACAAATCAGATCATGCCAGGACAGCTTCCTGATAATC 180
QY 181 ATCTGCGCCATAATCGCAAGAGAGGGGCGACTGTGCCCTGAGGAG 225
DB 181 ATCTGCGCCATAATCGCAAGAGAGGGGCGACTGTGCCCTGAGGAG 225

RESULT 4
US-08-967-727-18
Sequence 18, Application US/0896727
Patent No. 6025474
GENERAL INFORMATION:
APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,727
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,365
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6025474man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: MAGE-6 gene
US-08-967-727-18

Query Match 100.0%; Score 225; DB 3; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.4e-62;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATTCTTCTCTGATCTTCAGCAAGCTTCGGATTCCCTTGACAGCTGGTCTTTGGCATC 60
DB 1 TATTCTTCTCTGATCTTCAGCAAGCTTCGGATTCCCTTGACAGCTGGTCTTTGGCATC 60
QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCTGGGCTC 120
DB 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCTGGGCTC 120
QY 121 TCCTACCATGCGCTGCTGGGTGACAAATCAGATCATGCCAGGACAGCTTCCTGATAATC 180
DB 121 TCCTACCATGCGCTGCTGGGTGACAAATCAGATCATGCCAGGACAGCTTCCTGATAATC 180
QY 181 ATCTGCGCCATAATCGCAAGAGAGGGGCGACTGTGCCCTGAGGAG 225
DB 181 ATCTGCGCCATAATCGCAAGAGAGGGGCGACTGTGCCCTGAGGAG 225

RESULT 5
US-08-037-230B-18
Sequence 18, Application US/08037230D
Patent No. 6235525
GENERAL INFORMATION:
APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/037,230D
FILING DATE: 26-MARCH-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6235525man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: MAGE-6 gene
US-08-037-230D-18

Query Match 100.0%; Score 225; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 4.4e-62;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATTCTTTCTGTGATCTTCAGCAAAAGCTTCGGATTCCTTGCAGCTGGTCTTTGGCAATC 60
|||
Db 1 TATTCTTTCTGTGATCTTCAGCAAAAGCTTCGGATTCCTTGCAGCTGGTCTTTGGCAATC 60
|||

Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCACAGTGATACATCTTTGCCACCTGCTGGGCCTC 120
|||
Db 61 GAGCTGATGGAAGTGGACCCCATCGGCACAGTGATACATCTTTGCCACCTGCTGGGCCTC 120
|||

Qy 121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATATGCCCCAGGACAGGCTTCTGTATAATC 180
|||
Db 121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATATGCCCCAGGACAGGCTTCTGTATAATC 180
|||

Qy 181 ATCTGGCCATAATCGCAAGAGAGGGGCGACTGTGCCCTGAGGAG 225
|||
Db 181 ATCTGGCCATAATCGCAAGAGAGGGGCGACTGTGCCCTGAGGAG 225
|||

RESULT 6
US-09-056-105-7
; Sequence 7, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
; APPLICANT: KIPPS, THOMAS J.
; APPLICANT: WU, YUNQI
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
; TITLE OF INVENTION: PROCESSING
; FILE REFERENCE: 233/221
; CURRENT APPLICATION NUMBER: US/09/056,105
; CURRENT FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: 60/043,467
; EARLIER FILING DATE: 1997-04-10
; NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-056-105-7

Query Match 97.9%; Score 220.2; DB 4; Length 945;
Best Local Similarity 98.7%; Pred. No. 2.6e-60;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TATTCTTTCTGTGATCTTCAGCAAAAGCTTCGGATTCCTTGCAGCTGGTCTTTGGCAATC 60
|||
Db 433 tacttttctgtgatcttcagcaaaagcttcogattccttgacgtggtcttttggcatc 492
|||

Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCACAGTGATACATCTTTGCCACCTGCTGGGCCTC 120
|||
Db 493 gagctgatggaagtggaccccatcgccaagctgtacatctttgccacctgacctgggcctc 552
|||

Qy 121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATATGCCCCAGGACAGGCTTCTGTATAATC 180
|||
Db 553 tcctacgatggcctgctgggtgacaatcagatcatgcccgaagacaggtcttctgataatc 612
|||

Qy 181 ATCTGGCCATAATCGCAAGAGAGGGGCGACTGTGCCCTGAGGAG 225
|||
Db 613 atcctggccataatcgcaaaagagggcgactgtgccccctgaggag 657
|||

RESULT 7
US-09-056-105-13
; Sequence 13, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
; APPLICANT: KIPPS, THOMAS J.
; APPLICANT: WU, YUNQI
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
; TITLE OF INVENTION: PROCESSING
; FILE REFERENCE: 233/221
; CURRENT APPLICATION NUMBER: US/09/056,105
; CURRENT FILING DATE: 1998-04-06
; EARLIER APPLICATION NUMBER: 60/043,467
; EARLIER FILING DATE: 1997-04-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 1019
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-056-105-13

Query Match 97.9%; Score 220.2; DB 4; Length 1019;
Best Local Similarity 98.7%; Pred. No. 2.7e-60;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TATTCTTTCTGTGATCTTCAGCAAAAGCTTCGGATTCCTTGCAGCTGGTCTTTGGCAATC 60
|||
Db 498 tacttttctgtgatcttcagcaaaagcttcogattccttgacgtggtcttttggcatc 557
|||

Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCACAGTGATACATCTTTGCCACCTGCTGGGCCTC 120
|||
Db 558 gagctgatggaagtggaccccatcgccaagctgtacatctttgccacctgacctgggcctc 617
|||

Qy 121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATATGCCCCAGGACAGGCTTCTGTATAATC 180
|||
Db 618 tcctacgatggcctgctgggtgacaatcagatcatgcccgaagacaggtcttctgataatc 677
|||

Qy 181 ATCTGGCCATAATCGCAAGAGAGGGGCGACTGTGCCCTGAGGAG 225
|||
Db 678 atcctggccataatcgcaaaagagggcgactgtgccccctgaggag 722
|||

RESULT 8
US-08-993-738A-2
; Sequence 2, Application US/08993738A
; Patent No. 5928938
; GENERAL INFORMATION:
; APPLICANT: van der Bruggen, Pierre; DePlaen Etienne;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Complex With
; TITLE OF INVENTION: HLA-Cw*16 Molecules, and Uses Thereof
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,738A
; FILING DATE: 19-December-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/713,354
; FILING DATE: 13-September-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5928938man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5460.1 DIV - JEL/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1375 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-993-738A-2

Query Match 97.9%; Score 220.2; DB 2; Length 1375;
Best Local Similarity 98.7%; Pred. No. 3e-60;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TATTCTTTCTGTGATCTTCAGCAAGCTTCGAGTTCCGATTCCTTGGCAGCTGGTCTTTGGCATC 60
Db 592 TACTTCTTTCTGTGATCTTCAGCAAGCTTCGAGTTCCGATTCCTTGGCAGCTGGTCTTTGGCATC 651
QY 61 GAGCTGATGGAAGTGGAGCCCATCGGCCACGCTGTACATCTTTGCCACCTGCCTGGGCCTC 120
Db 652 GAGCTGATGGAAGTGGAGCCCATCGGCCACGCTGTACATCTTTGCCACCTGCCTGGGCCTC 711
QY 121 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCCCAGGACAGCTTCCTGTATAATC 180
Db 712 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCCCAGGACAGCTTCCTGTATAATC 771
QY 181 ATCTGTGCCATAATCGCAAGAGGGGCGACTGTGCCCTGAGGAG 225
Db 772 ATCTGTGCCATAATCGCAAGAGGGGCGACTGTGCCCTGAGGAG 816

RESULT 9
US-08-713-354C-2
; Sequence 2, Application US/08713354C
; Patent No. 6265215
; GENERAL INFORMATION:
; APPLICANT: van der Bruggen, Pierre; DePlaen Etienne;

; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Complex With
; TITLE OF INVENTION: HLA-Cw*16 Molecules, and Uses Thereof
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,354C
; FILING DATE: 13-September-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6265215man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5460
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1375 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-713-354C-2

Query Match 97.9%; Score 220.2; DB 4; Length 1375;
Best Local Similarity 98.7%; Pred. No. 3e-60;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TATTCTTTCTGTGATCTTCAGCAAGCTTCGAGTTCCGATTCCTTGGCAGCTGGTCTTTGGCATC 60
Db 592 TACTTCTTTCTGTGATCTTCAGCAAGCTTCGAGTTCCGATTCCTTGGCAGCTGGTCTTTGGCATC 651
QY 61 GAGCTGATGGAAGTGGAGCCCATCGGCCACGCTGTACATCTTTGCCACCTGCCTGGGCCTC 120
Db 652 GAGCTGATGGAAGTGGAGCCCATCGGCCACGCTGTACATCTTTGCCACCTGCCTGGGCCTC 711
QY 121 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCCCAGGACAGCTTCCTGTATAATC 180
Db 712 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCCCAGGACAGCTTCCTGTATAATC 771
QY 181 ATCTGTGCCATAATCGCAAGAGGGGCGACTGTGCCCTGAGGAG 225
Db 772 ATCTGTGCCATAATCGCAAGAGGGGCGACTGTGCCCTGAGGAG 816

RESULT 10
US-07-807-043B-11
; Sequence 11, Application US/07807043B
; Patent No. 5342774
; GENERAL INFORMATION:
; APPLICANT: Boon, Thierry, Van den Eynde, Beno t
; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
; TITLE OF INVENTION: Rejection Antigens and Uses Thereof
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/807,043B
FILING DATE: 19911212
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-May-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5342774man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 253.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1640 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: singular
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
FEATURE:
NAME/KEY: CDNA MAGE-3
US-07-807-043B-11

Query Match 95.0%; Score 213.8; DB 1; Length 1640;
Best Local Similarity 96.9%; Pred. No. 3.4e-58;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCCGATTCCTTGACGCTGGTCTTTGGCATC 60
Db 604 TATTTCTTCTGTGATCTTCAGCAAGCTTCCAGTTCCTTGACGCTGGTCTTTGGCATC 663
Qy 61 GAGCTGATGGAAGTGGAGCCCATCGGACAGTGATACATCTTTGGCACCTGCTGGGCCTC 120
Db 664 GAGCTGATGGAAGTGGAGCCCATCGGACAGTGATACATCTTTGGCACCTGCTGGGCCTC 723
Qy 121 TCCTACGATGGCTGCTGGTGACAAATCAGATCATGCCACGACAGGCTTCTGTGATAATC 180
Db 724 TCCTACGATGGCTGCTGGTGACAAATCAGATCATGCCACGACAGGCTTCTGTGATAATC 783
Qy 181 ATCTTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGTAGGAG 225
Db 784 GTCTTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGTAGGAG 828

RESULT 11
US-08-299-849B-11
Sequence 11, Application US/08299849B
Patent No. 5612201
GENERAL INFORMATION:
APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
APPLICANT: Chomez, Patrick
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felie & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,849B
FILING DATE: 1-SEPTEMBER-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-May-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5612201man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5355
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1640 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
FEATURE:
NAME/KEY: CDNA MAGE-3
US-08-299-849B-11

Query Match 95.0%; Score 213.8; DB 1; Length 1640;
Best Local Similarity 96.9%; Pred. No. 3.4e-58;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCCGATTCCTTGACGCTGGTCTTTGGCATC 60
Db 604 TATTTCTTCTGTGATCTTCAGCAAGCTTCCAGTTCCTTGACGCTGGTCTTTGGCATC 663
Qy 61 GAGCTGATGGAAGTGGAGCCCATCGGACAGTGATACATCTTTGGCACCTGCTGGGCCTC 120
Db 664 GAGCTGATGGAAGTGGAGCCCATCGGACAGTGATACATCTTTGGCACCTGCTGGGCCTC 723
Qy 121 TCCTACGATGGCTGCTGGTGACAAATCAGATCATGCCACGACAGGCTTCTGTGATAATC 180
Db 724 TCCTACGATGGCTGCTGGTGACAAATCAGATCATGCCACGACAGGCTTCTGTGATAATC 783
Qy 181 ATCTTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGTAGGAG 225
Db 784 GTCTTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGTAGGAG 828

RESULT 12
US-08-142-368A-11
Sequence 11, Application US/08142368A
Patent No. 5925729
GENERAL INFORMATION:
APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry;

APPLICANT: Van den Eynde, Beno t; Van Pel, Aline; De plaen, Etienne;
APPLICANT: Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
TITLE OF INVENTION: Rejection Antigens and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,368A
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5925729man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5253.4-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1640 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna to mRNA
NAME/KEY: cdna MAGE-3
US-08-142-368A-11

Query Match 95.0%; Score 213.8; DB 2; Length 1640;
Best Local Similarity 96.9%; Pred. No. 3.4e-58;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 TATTCTTTCTCTGTGATCTTCAGCAAGCTTCGATTCCTTGCAGCTGGTCTTTGGCATC 60
Db 604 TATTCTTTCTCTGTGATCTTCAGCAAGCTTCGATTCCTTGCAGCTGGTCTTTGGCATC 663
QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACTTCCTCGGGCCTC 120
Db 664 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACTTCCTCGGGCCTC 723
QY 121 TCCTACGATGGCCTGCTGGGTGACAAATCAGATCATGCCAGGACGCTTCCTGATAATC 180
Db 724 TCCTACGATGGCCTGCTGGGTGACAAATCAGATCATGCCAGGACGCTTCCTGATAATC 783
QY 181 ATCTGCGCCATATCGCAAGAGAGGGGACTGTGCCCCCTGAGGAG 225
Db 784 GTCTGCGCCATATCGCAAGAGAGGGGACTGTGCCCCCTGAGGAG 828

RESULT 13
US-08-967-727-11
Sequence 11, Application US/08967727
Patent No. 6025474
GENERAL INFORMATION:
APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,727
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,365
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6025474man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1640 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna to mRNA
FEATURE:
NAME/KEY: cdna MAGE-3
US-08-967-727-11

Query Match 95.0%; Score 213.8; DB 3; Length 1640;
Best Local Similarity 96.9%; Pred. No. 3.4e-58;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 TATTCTTTCTCTGTGATCTTCAGCAAGCTTCGATTCCTTGCAGCTGGTCTTTGGCATC 60
Db 604 TATTCTTTCTCTGTGATCTTCAGCAAGCTTCGATTCCTTGCAGCTGGTCTTTGGCATC 663
QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACTTCCTCGGGCCTC 120

Db 664 GAGCTGATGGAAGTGGACCCCATCGGCACCTGTACATCTTTGCCACCTGCTGGGCTC 723
 QY 121 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 180
 Db 724 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 783
 QY 181 ATCTGTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCCCTGAGGAG 225
 Db 784 GTCTGTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCCCTGAGGAG 828

RESULT 14
 US-08-037-230D-11
 ; Sequence 11, Application US/08037230D
 ; Patent No. 6235525
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
 ; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
 ; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
 ; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Felfe & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York City
 ; STATE: New York
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 ; COMPUTER: IBM
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: Wordperfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/037,230D
 ; FILING DATE: 26-MARCH-1993
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US92/04354
 ; FILING DATE: 22-MAY-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/807,043
 ; FILING DATE: 12-DECEMBER-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/764,364
 ; FILING DATE: 23-SEPTEMBER-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/728,838
 ; FILING DATE: 9-JULY-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/705,702
 ; FILING DATE: 23-MAY-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hanson, No. 6235525man D.
 ; REGISTRATION NUMBER: 30,946
 ; REFERENCE/DOCKET NUMBER: LUD 5353
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 688-9200
 ; TELEFAX: (212) 838-3884
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1640 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cdna to mrna
 ; FEATURE:
 ; NAME/KEY: CDNA MAGE-3
 ; US-08-037-230D-11

Query Match 95.0%; Score 213.8; DB 4; Length 1640;
 Best Local Similarity 96.9%; Pred. No. 3.4e-58;
 Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTTCTTTCTGTGATCTTTTCAGCAAAAGCTTCCGATTTCCCTTGAGCGTGTCTTTGGCATC 60
 Db 604 TATTTCTTTCTGTGATCTTTTCAGCAAAAGCTTCCGATTTCCCTTGAGCGTGTCTTTGGCATC 663
 QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTTGTACATCTTTGCCACCTGCTGGGCTC 120
 Db 664 GAGCTGATGGAAGTGGACCCCATCGGCACGTTGTACATCTTTGCCACCTGCTGGGCTC 723
 QY 121 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 180
 Db 724 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 783
 QY 181 ATCTGTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCCCTGAGGAG 225
 Db 784 GTCTGTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCCCTGAGGAG 828

RESULT 15
 US-08-928-615-1
 ; Sequence 1, Application US/08928615
 ; Patent No. 5965535
 ; GENERAL INFORMATION:
 ; APPLICANT: Chaux, Pascal
 ; APPLICANT: Stroobant, Vincent
 ; APPLICANT: Boon, Thierry
 ; APPLICANT: van der Bruggen, Pierre
 ; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED
 ; TITLE OF INVENTION: BY HLA CLASS II MOLECULES
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 ; STREET: 600 Atlantic Avenue
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: U.S.A.
 ; ZIP: 02210-2211
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/928,615
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Van Amsterdam, John R.
 ; REGISTRATION NUMBER: 40,212
 ; REFERENCE/DOCKET NUMBER: L0461/7017
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-720-3500
 ; TELEFAX: 617-720-2441
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4204 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cdna
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FEATURE:
 ; NAME/KEY: Coding Sequence
 ; LOCATION: 2465...3406
 ; US-08-928-615-1

Query Match 95.0%; Score 213.8; DB 2; Length 4204;
 Best Local Similarity 96.9%; Pred. No. 5e-58;
 Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTTCTTTCTGTGATCTTTTCAGCAAAAGCTTCCGATTTCCCTTGAGCGTGTCTTTGGCATC 60

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Db 2897 TATTTCTTTTCCTGTGATCTTCAGCAAGCTTCAGTTCCCTTGAGCTGGTCTTTGGCATC 2956
QY 61 GAGCTGATGGAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGGCTGGCCCTC 120
Db 2957 GAGCTGATGGAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGGCTGGCCCTC 3016
QY 121 TCCTACGATGGCCCTGCTGGGTGACAATCAGATCATGCCCCAGGACAGGCTTCCTGATAATC 180
Db 3017 TCCTACGATGGCCCTGCTGGGTGACAATCAGATCATGCCCCAGGACAGGCTTCCTGATAATC 3076
QY 181 ATCCTGGCCATAATCGCAAGAGAGGGGAGTGTGCCCTGAGGAG 225
Db 3077 GTCCCTGGCCATAATCGCAAGAGAGGGGAGTGTGCCCTGAGGAG 3121
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Search completed: September 4, 2002, 21:15:19
Job time: 20229 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 4, 2002, 10:40:10 ; Search time 1028.98 Seconds
(without alignments)
1660.387 Million cell updates/sec

Title: US-08-967-727-18

Perfect score: 225

Sequence: 1 TATTCTTCTCTGATCTT.....GCGACTGTGCCCTGAGGAG 225

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:.*
2: em_esthum:.*
3: em_estin:.*
4: em_estmu:.*
5: em_estov:.*
6: em_estpl:.*
7: em_estro:.*
8: em_htc:.*
9: gb_est1:.*
10: gb_est2:.*
11: gb_htc:.*
12: gb_gss:.*
13: em_gss_hum:.*
14: em_gss_inv:.*
15: em_gss_pln:.*
16: em_gss_vrt:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	220.2	97.9	563	10	BG477228
2	220.2	97.9	776	10	BG476912
3	220.2	97.9	876	10	BF792356
4	220.2	97.9	878	10	BG397171
5	220.2	97.9	886	10	BG476078
6	213.8	95.0	623	10	BF793889
7	213.8	95.0	686	10	BG575715
8	213.8	95.0	704	10	BT090658
9	213.8	95.0	769	10	BG765526
10	213.8	95.0	872	10	BM449726
11	212.8	94.6	1021	10	BM470991
12	202.6	90.0	934	10	BG280738
13	201.4	89.5	795	10	BE541476
14	197.6	87.8	803	10	BM015882
15	196.8	87.5	590	10	BE897495
16	196.8	87.5	680	10	BE563063
17	196.4	87.3	768	10	BI086876

18	196	87.1	767	10	BI092532
19	195.8	87.0	1114	10	BM479202
20	195.2	86.8	1089	10	BG029985
21	194.8	86.6	809	10	BI855745
22	194	86.2	707	10	BG760839
23	193.6	86.0	484	10	BF970108
24	193.6	86.0	784	10	BF793468
25	178.8	79.5	845	10	BG481937
26	176.8	78.6	894	10	BG765817
27	165.4	73.5	810	9	AL526639
28	164.6	73.2	816	10	BI086919
29	163.4	72.6	797	10	BI087493
30	162.8	72.4	929	10	BE896896
31	159.6	70.9	962	10	BG116297
32	159.6	70.9	1050	10	BG024106
33	156.4	69.5	956	10	BE900736
34	154.8	68.8	876	10	BE795782
35	153.2	68.1	929	10	BE275276
36	152.8	67.9	704	10	BG764972
37	150.2	66.8	845	10	BI089076
38	148.8	66.1	716	10	BM015975
39	147.6	65.6	922	10	BG115115
40	147.6	65.6	946	10	BE983819
41	146	64.9	948	9	AL562721
42	143.4	63.7	941	10	BI830314
43	141.8	63.0	820	10	BG481340
44	138.6	61.6	1109	10	BG333682
45	138.2	61.4	597	10	BE281072

ALIGNMENTS

RESULT 1

BG477228

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BG477228 563 bp mRNA linear EST 21-MAR-2001
60252437F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4642641 5',
mRNA sequence.
BG477228
BG477228.1 GI:13409507
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 563)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW411 row: i column: 10
High quality sequence stop: 499.
Location/Qualifiers
1. .563
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NIH_MGC_20"
/lissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in

FEATURES
source

the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT
ORIGIN

Query Match 97.9%; Score 220.2; DB 10; Length 563;
Best Local Similarity 98.7%; Pred. No. 3.5e-48;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTTCCTTCCTGATCTTCAGCAAGCTTCCGATTCCTTGACGCTGGCTTTGGGCATC 60
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Db 191 TACTTCCTTCCTGATCTTCAGCAAGCTTCCGATTCCTTGACGCTGGCTTTGGGCATC 250
|||
QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGCTGTACATCTTTGCCACCTGCTGGGCCTC 120
|||
Db 251 GAGCTGATGGAAGTGGACCCCATCGGCACGCTGTACATCTTTGCCACCTGCTGGGCCTC 310
|||
QY 121 TCCTACGATGCCCTGCTGGTGGTGAACAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 180
|||
Db 311 TCCTACGATGCCCTGCTGGTGGTGAACAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 370
|||

QY 181 ATCTGCGCCATAATCGCAAGAGGGCGACTGTGCCCTGAGGAG 225
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Db 371 ATCTGCGCCATAATCGCAAGAGGGCGACTGTGCCCTGAGGAG 415
|||||

RESULT 2

BF792356 776 bp mRNA linear EST 21-MAR-2001
LOCUS 602524881F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4642868 5',
DEFINITION mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

BF792356
BF792356.1 GI:13409178
EST
human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 776)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1CM1412 row: b column: 21

High quality sequence stop: 747.

Location/Qualifiers

FEATURES

source

1..776

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4642868"

/clone_lib="NIH_MGC_20"

/tissue_type="melanotic melanoma"

/lab_host="DH10B (phage-resistant)"

/note="organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCAGGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

180 a 197 c 232 g 167 t

BASE COUNT
ORIGIN

Query Match 97.9%; Score 220.2; DB 10; Length 876;
Best Local Similarity 98.7%; Pred. No. 3.9e-48;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTTCCTTCCTGATCTTCAGCAAGCTTCCGATTCCTTGACGCTGGCTTTGGGCATC 60
|||||

Query Match 97.9%; Score 220.2; DB 10; Length 776;
Best Local Similarity 98.7%; Pred. No. 3.8e-48;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTTCCTTCCTGATCTTCAGCAAGCTTCCGATTCCTTGACGCTGGCTTTGGGCATC 60
|||
Db 191 TACTTCCTTCCTGATCTTCAGCAAGCTTCCGATTCCTTGACGCTGGCTTTGGGCATC 250
|||
QY 61 GAGCTGATGGAAGTGGACCCCATCGGCACGCTGTACATCTTTGCCACCTGCTGGGCCTC 120
|||
Db 251 GAGCTGATGGAAGTGGACCCCATCGGCACGCTGTACATCTTTGCCACCTGCTGGGCCTC 310
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QY 121 TCCTACGATGCCCTGCTGGTGGTGAACAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 180
|||
Db 311 TCCTACGATGCCCTGCTGGTGGTGAACAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 370
|||
QY 181 ATCTGCGCCATAATCGCAAGAGGGCGACTGTGCCCTGAGGAG 225
|||||
Db 371 ATCTGCGCCATAATCGCAAGAGGGCGACTGTGCCCTGAGGAG 415
|||||

RESULT 3

BF792356 876 bp mRNA linear EST 12-JAN-2001
LOCUS 60252896F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4345222 5',
DEFINITION mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

BF792356
BF792356.1 GI:12097410
EST
human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 876)

NIH-MGC <http://mgi.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L1AM9964 row: p column: 23

High quality sequence stop: 780.

Location/Qualifiers

FEATURES

source

1..876

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4345222"

/clone_lib="NIH_MGC_84"

/tissue_type="adrenal cortex carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:

NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT

primed. Average insert size 1.229 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH_MGC Library."

185 a 215 c 248 g 228 t

BASE COUNT

ORIGIN

Query Match 97.9%; Score 220.2; DB 10; Length 876;
Best Local Similarity 98.7%; Pred. No. 3.9e-48;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTTCCTTCCTGATCTTCAGCAAGCTTCCGATTCCTTGACGCTGGCTTTGGGCATC 60
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Db 78 TATTCTTTCCCTGTGATCTTCATCAAGCTTCGGATTCCCTGCGTGGTCTTTGGCATC 137
QY 61 GAGCTGATGAAGTGACCCCATCGGCCACGCTGTACATCTTTGCCACCTGCGCTGGGCCCTC 120
Db 138 GAGCTGATGAAGTGACCCCATCGGCCACGCTGTACATCTTTGCCACCTGCGCTGGGCCCTC 197
QY 121 TCCTAGCATGGCTGCTGGGTGACATCAATCAGATCATGCCCAGGACAGCTTCCCTGATAATC 180
Db 198 TCCTAGCATGGCTGCTGGGTGACATCAATCAGATCATGCCCAGGACAGCTTCCCTGATAATC 257
QY 181 ATCCCTGCCATATCCCAAGAGAGCGGCGACTGTGCCCTGAGGAG 225
Db 258 ATCCCTGCCATATCCCAAGAGAGCGGCGACTGTGCCCTGAGGAG 302

RESULT 4
BG397171
LOCUS BG397171 878 bp mRNA linear EST 12-MAR-2001
DEFINITION 602434130F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4552086 5',
mRNA sequence.
ACCESSION BG397171
VERSION BG397171.1 GI:13290619
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 878)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM1247 row: 1 column: 07
High quality sequence stop: 866.
FEATURES
Location/Qualifiers
1..878
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4552086"
/clone_lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 197 a 214 c 262 g 205 t
ORIGIN

Query Match 97.9%; Score 220.2; DB 10; Length 878;
Best Local Similarity 98.7%; Pred. No. 3.9e-48;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTCTTTCCCTGTGATCTTCAGCAAGCTTCGGATTCCCTGCGTGGTCTTTGGCATC 60
Db 190 TACTTCTTCCCTGTGATCTTCAGCAAGCTTCGGATTCCCTGCGTGGTCTTTGGCATC 249
QY 61 GAGCTGATGAAGTGACCCCATCGGCCACGCTGTACATCTTTGCCACCTGCGCTGGGCCCTC 120
Db 250 GAGCTGATGAAGTGACCCCATCGGCCACGCTGTACATCTTTGCCACCTGCGCTGGGCCCTC 309
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QY 121 TCCTAGCATGGCTGCTGGGTGACAAATCAGATCATGCCCAGGACAGCTTCCCTGATAATC 180
Db 310 TCCTAGCATGGCTGCTGGGTGACAAATCAGATCATGCCCAGGACAGCTTCCCTGATAATC 369
QY 181 ATCCTGGCCATATCCCAAGAGAGCGGCGACTGTGCCCTGAGGAG 225
Db 370 ATCCTGGCCATATCCCAAGAGAGCGGCGACTGTGCCCTGAGGAG 414

RESULT 5
BG476078
LOCUS BG476078 886 bp mRNA linear EST 21-MAR-2001
DEFINITION 602520963F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4639670 5',
mRNA sequence.
ACCESSION BG476078
VERSION BG476078.1 GI:13408357
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 886)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM1403 row: m column: 15
High quality sequence stop: 730.
FEATURES
Location/Qualifiers
1..886
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/db_xref="taxon:9606"
/clone="IMAGE:4639670"
/clone_lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 183 a 231 c 262 g 210 t
ORIGIN
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Query Match 97.9%; Score 220.2; DB 10; Length 886;
Best Local Similarity 98.7%; Pred. No. 3.9e-48;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTCTTTCCCTGTGATCTTCAGCAAGCTTCGGATTCCCTGCGTGGTCTTTGGCATC 60
Db 94 TACTTCTTCCCTGTGATCTTCAGCAAGCTTCGGATTCCCTGCGTGGTCTTTGGCATC 153
QY 61 GAGCTGATGAAGTGACCCCATCGGCCACGCTGTACATCTTTGCCACCTGCGCTGGGCCCTC 120
Db 154 GAGCTGATGAAGTGACCCCATCGGCCACGCTGTACATCTTTGCCACCTGCGCTGGGCCCTC 213
QY 121 TCCTAGCATGGCTGCTGGGTGACAAATCAGATCATGCCCAGGACAGCTTCCCTGATAATC 180
Db 214 TCCTAGCATGGCTGCTGGGTGACAAATCAGATCATGCCCAGGACAGCTTCCCTGATAATC 273
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Qy 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTCCCTGAGGAG 225
|||||
Db 274 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTCCCTGAGGAG 318
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RESULT 6
BF793889
LOCUS 60225285f1 NIH_MGC_84 623 bp mRNA linear EST 12-JAN-2001
DEFINITION 60225285f1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4347380 5',
mRNA sequence.
ACCESSION BF793889
VERSION BF793889.1 GI:12098943
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 623)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9970 row: j column: 21
High quality sequence stop: 622.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4347380"
/tissue_type="adrenal cortex carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
Noti; Site_2: SalI; Cloned unidirectionally; oligo-dT
primed. Average insert size 1.229 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 136 a 173 c 177 g 137 t
ORIGIN

Query Match 95.0%; Score 213.8; DB 10; Length 623;
Best Local Similarity 96.9%; Pred. No. 1.8e-46;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TATTTCTTCTGTGATCTTCAGCAAGCTCCGATCTTGTGACGTGGTCTTTGGCATC 60
|||||
Db 326 TATTTCTTCTGTGATCTTCAGCAAGCTTCAGTCTTGTGACGTGGTCTTTGGCATC 385
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Qy 61 GAGCTGATGGAAGTGGACCCATCGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120
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Db 386 GAGCTGATGGAAGTGGACCCATCGCCACCTGTGATCATCTTTGCCACCTGCCTGGGCCTC 445
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Qy 121 TCCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCACGACAGGCTTCTGTATATC 180
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Db 446 TCCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCACGACAGGCTTCTGTATATC 505
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Qy 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTCCCTGAGGAG 225
|||||
Db 506 GTCTGGCCATAATCGCAAGAGAGGGCGACTGTCCCTGAGGAG 550
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RESULT 7
BG575715
LOCUS 602853894f1 NIH_MGC_10 704 bp mRNA linear EST 20-JUN-2001
DEFINITION 602853894f1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4995238 5',
mRNA sequence.
ACCESSION BI090658
VERSION BI090658.1 GI:14508988
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 704)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Prepared by: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11018 row: 1 column: 23
High quality sequence stop: 703.

FEATURES
Location/Qualifiers
1..704
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4995238"
/clone_lib="NIH_MGC_10"
/cell_line="MGC36"
/lab_host="DH10B"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5 kb. Library prepared by Life
Technologies."

BASE COUNT 158 a 174 c 214 g 157 t 1 others
ORIGIN

Query Match 95.0%; Score 213.8; DB 10; Length 704;
Best Local Similarity 96.9%; Pred. No. 1.8e-46;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCTTCCTGCGAGTGGTCTTTGGCATC 60
|||||
Db 154 TATTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCTTCCTGCGAGTGGTCTTTGGCATC 213
|||||

QY 61 GAGCTGATGGAAGTGACCCCATCGCCAGGTCATCATGCCAGGACAGCTTCCTGTGATAATC 120
|||||
Db 214 GAGCTGATGGAAGTGACCCCATCGCCAGGTCATCATGCCAGGACAGCTTCCTGTGATAATC 273
|||||

QY 121 TCCTAGATGGCTGCTGGTGTACATCAGATCATGCCAGGACAGCTTCCTGTGATAATC 180
|||||
Db 274 TCCTAGATGGCTGCTGGTGTACATCAGATCATGCCAGGACAGCTTCCTGTGATAATC 333
|||||

QY 181 ATCTGGCCATATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
|||||
Db 334 GTCTGGCCATATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 378
|||||

RESULT 9
BG765526
LOCUS
DEFINITION 602739439F1 NIH_MGC_49 Homo sapiens cdna clone IMAGE:4869321 5',
mrna sequence.
ACCESSION BG765526
VERSION BG765526.1 GI:14076179
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 769)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory

Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 704)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Prepared by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11018 row: 1 column: 23
High quality sequence stop: 703.

FEATURES
Location/Qualifiers
1..704
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4995238"
/clone_lib="NIH_MGC_10"
/cell_line="MGC36"
/lab_host="DH10B"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5 kb. Library prepared by Life
Technologies."

BASE COUNT 158 a 174 c 214 g 157 t 1 others
ORIGIN

Query Match 95.0%; Score 213.8; DB 10; Length 704;
Best Local Similarity 96.9%; Pred. No. 1.8e-46;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCTTCCTGCGAGTGGTCTTTGGCATC 60
|||||
Db 154 TATTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCTTCCTGCGAGTGGTCTTTGGCATC 213
|||||

QY 61 GAGCTGATGGAAGTGACCCCATCGCCAGGTCATCATGCCAGGACAGCTTCCTGTGATAATC 120
|||||
Db 214 GAGCTGATGGAAGTGACCCCATCGCCAGGTCATCATGCCAGGACAGCTTCCTGTGATAATC 273
|||||

QY 121 TCCTAGATGGCTGCTGGTGTACATCAGATCATGCCAGGACAGCTTCCTGTGATAATC 180
|||||
Db 274 TCCTAGATGGCTGCTGGTGTACATCAGATCATGCCAGGACAGCTTCCTGTGATAATC 333
|||||

QY 181 ATCTGGCCATATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
|||||
Db 334 GTCTGGCCATATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 378
|||||

RESULT 9
BG765526
LOCUS
DEFINITION 602739439F1 NIH_MGC_49 Homo sapiens cdna clone IMAGE:4869321 5',
mrna sequence.
ACCESSION BG765526
VERSION BG765526.1 GI:14076179
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 769)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM1740 row: n column: 10
High quality sequence stop: 769.

FEATURES
Location/Qualifiers
1..769
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4869321"
/clone_lib="NIH_MGC_49"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

BASE COUNT 161 a 218 c 222 g 168 t
ORIGIN

Query Match 95.0%; Score 213.8; DB 10; Length 769;
Best Local Similarity 96.9%; Pred. No. 1.8e-46;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCTTCCTGCGAGTGGTCTTTGGCATC 60
|||||
Db 374 TATTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCTTCCTGCGAGTGGTCTTTGGCATC 433
|||||

QY 61 GAGCTGATGGAAGTGACCCCATCGCCAGGTCATCATGCCAGGACAGCTTCCTGTGATAATC 120
|||||
Db 434 GAGCTGATGGAAGTGACCCCATCGCCAGGTCATCATGCCAGGACAGCTTCCTGTGATAATC 493
|||||

QY 121 TCCTAGATGGCTGCTGGTGTACATCAGATCATGCCAGGACAGCTTCCTGTGATAATC 180
|||||
Db 494 TCCTAGATGGCTGCTGGTGTACATCAGATCATGCCAGGACAGCTTCCTGTGATAATC 553
|||||

QY 181 ATCTGGCCATATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
|||||
Db 554 GTCTGGCCATATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 598
|||||

RESULT 10
BM449726
LOCUS
DEFINITION 6392873 NIH_MGC_72 Homo sapiens cdna clone IMAGE:5528433
5', mRNA sequence.
ACCESSION BM449726
VERSION BM449726.1 GI:18498766
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 872)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/BTP
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LHAM12205 row: e column: 10
High quality sequence stop: 668.
Location/Qualifiers

FEATURES

source 1..872

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5528433"
/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-Sport6; Site:1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

BASE COUNT 186 a 255 c 249 g 182 t
ORIGIN

Query Match 95.0%; Score 213.8; DB 10; Length 872;
Best Local Similarity 96.9%; Pred. No. 1.9e-46;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTCTTCTGTCATCTTCAGCAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60
|||||
Db 507 TATTCTTCTGTCATCTTCAGCAAGCTTCCAGTTCCTTGCAGCTGGTCTTTGGCATC 566
|||||

QY 61 GAGCTGATGGAAGTGACCCCATCGGCACGCTGTACATCTTTGGCACCCTGCTGGGCCTC 120
|||||
Db 567 GAGCTGATGGAAGTGACCCCATCGGCACCTTCCACTTTTGCACCTGCTGGGCCTC 626
|||||

QY 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGCAGAGGCTTCTGTATATC 180
Db 627 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGCAGAGGCTTCTGTATATC 686
|||||

QY 181 ATCTGGCCATAATCGCAAGAGAGGGGACCTGTGCCCTGAGGAG 225
|||||
Db 687 GTCTGGCCATAATCGCAAGAGAGGGGACCTGTGCCCTGAGGAG 731
|||||

RESULT 11

BM470991 1021 bp mRNA linear EST 05-FEB-2002
LOCUS BM470991.1 GI:18520033
DEFINITION AGENCOURT_6478212 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5562971
5', mRNA sequence.
ACCESSION BM470991
VERSION BM470991.1
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1021)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM12293 row: d column: 12
High quality sequence stop: 725.
Location/Qualifiers

FEATURES source

1..1021
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5562971"
/clone_lib="NIH_MGC_72"

/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-Sport6; Site:1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

BASE COUNT 232 a 290 c 292 g 206 t 1 others
ORIGIN

Query Match 94.6%; Score 212.8; DB 10; Length 1021;
Best Local Similarity 96.4%; Pred. No. 3.7e-46;
Matches 217; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 TATTCTTCTGTCATCTTCAGCAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 60
|||||
Db 593 TACTTCTTCTGTCATCTTCAGCAAGCTTCCGATTCCTTGCAGCTGGTCTTTGGCATC 652
|||||

QY 61 GAGCTGATGGAAGTGACCCCATCGGCACGCTGTACATCTTTGCCACCTGCTGGGCCTC 120
|||||
Db 653 GAGCTGATGGAAGTGACCCCATCGGCACGCTGTACATCTTTGCCACCTGCTGGGCCTC 712
|||||

QY 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGCAGAGGCTTCTGTATATC 180
Db 713 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGCAGAGGCTTCTGTATATC 772
|||||

QY 181 ATCTGGCCATAATCGCAAGAGAGGGGACCTGTGCCCTGAGGAG 225
|||||
Db 773 ATCTGGCCATAATCGCAAGAGAGGGGACCTGTGCCCTGAGGAG 817
|||||

RESULT 12

BM4709738 934 bp mRNA linear EST 21-FEB-2001
LOCUS BM4709738.1 GI:13029662
DEFINITION 602401029F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4543566 5',
mRNA sequence.
ACCESSION BM4709738
VERSION BM4709738.1
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 934)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LHAM1225 row: 1 column: 07
High quality sequence stop: 673.
Location/Qualifiers

FEATURES source

1..934
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4543566"
/clone_lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site:1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

```
BASE COUNT      235 a      266 c      267 g      166 t
ORIGIN
Query Match      90.0%; Score 202.6; DB 10; Length 934;
Best Local Similarity 95.9%; Pred. No. 1.8e-43;
Matches 208; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 TATTCTTCTCTGATCTTCAGCAAGCTTCGGATTCTTCAGCTGGTCTTTGGCATC 60
Db 418 TATTCTTCTCTGATCTTCAGCAAGCTTCAGTCTCTTCAGCTGGTCTTTGGCATC 477

QY 61 GAGCTGATGAAGTGAACCCATCGCCAGTGTACATCTTTGCCACCTGCCCTGGCCCTC 120
Db 478 GAGCTGATGAAGTGAACCCATCGCCAGTGTACATCTTTGCCACCTGCCCTGGCCCTC 537

QY 121 TCCTACGATGGCTGCTGGGTGACATCAGATCATGCCAGACAGCTTCCTGTATAATC 180
Db 538 TCCTACGATGGACTGCTGGGTGACATCAGATCATGCCAAGCAGCGCTTCCTGTATAATC 597

QY 181 ATCTCGGCCATAATCGCAAGAGAGGGCGACTGTGCC 217
Db 598 GTCTGCGCCATAATCGCAAGAGAGGGCGACTGTGCC 634

RESULT 13
BE541476
LOCUS      BE541476      795 bp      mRNA      linear      EST 09-AUG-2000
DEFINITION 601067928F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454135 5',
            mRNA sequence.
ACCESSION  BE541476
VERSION    BE541476.1 GI:9770121
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 795)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-remail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM8438 row: h column: 08
            High quality sequence stop: 662.
FEATURES   Location/Qualifiers
            source      1..795
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:3454135"
                        /clone_lib="NIH_MGC_10"
                        /cell_line="MGC36"
                        /lab_host="DH10B"
                        /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
                        Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                        Average insert size 1.5 kb. Library prepared by Life
                        Technologies."
BASE COUNT  182 a      199 c      234 g      180 t
ORIGIN
Query Match      89.5%; Score 201.4; DB 10; Length 795;
Best Local Similarity 96.9%; Pred. No. 3.5e-43;
Matches 216; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 3 TTTCTTCTCTGATCTTCAGCAAGCTTCGGATTCTTCGAGCTGGTCTTTGGCATCGA 62

BASE COUNT      235 a      266 c      267 g      166 t
ORIGIN
Query Match      90.0%; Score 202.6; DB 10; Length 934;
Best Local Similarity 95.9%; Pred. No. 1.8e-43;
Matches 208; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 TATTCTTCTCTGATCTTCAGCAAGCTTCGGATTCTTCAGCTGGTCTTTGGCATC 60
Db 418 TATTCTTCTCTGATCTTCAGCAAGCTTCAGTCTCTTCAGCTGGTCTTTGGCATC 477

QY 61 GAGCTGATGAAGTGAACCCATCGCCAGTGTACATCTTTGCCACCTGCCCTGGCCCTC 120
Db 478 GAGCTGATGAAGTGAACCCATCGCCAGTGTACATCTTTGCCACCTGCCCTGGCCCTC 537

QY 121 TCCTACGATGGCTGCTGGGTGACATCAGATCATGCCAGACAGCTTCCTGTATAATC 180
Db 538 TCCTACGATGGACTGCTGGGTGACATCAGATCATGCCAAGCAGCGCTTCCTGTATAATC 597

QY 181 ATCTCGGCCATAATCGCAAGAGAGGGCGACTGTGCC 217
Db 598 GTCTGCGCCATAATCGCAAGAGAGGGCGACTGTGCC 634

RESULT 14
BM015882
LOCUS      BM015882      803 bp      mRNA      linear      EST 30-OCT-2001
DEFINITION 603642276F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5418283 5',
            mRNA sequence.
ACCESSION  BM015882
VERSION    BM015882.1 GI:16530236
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 803)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-remail.nih.gov
            Tissue Procurement: DCTD/DTF
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12067 row: g column: 20
            High quality sequence stop: 779.
FEATURES   Location/Qualifiers
            source      1..803
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:5418283"
                        /clone_lib="NIH_MGC_87"
                        /tissue_type="mammary adenocarcinoma, cell line"
                        /lab_host="DH10B (phage-resistant)"
                        /note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
                        Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                        Average insert size 1.383 kb. Library enriched for
                        full-length clones and constructed by Life Technologies.
                        Note: this is a NIH_MGC library."
BASE COUNT  169 a      236 c      236 g      161 t
ORIGIN
Query Match      87.8%; Score 197.6; DB 10; Length 803;
Best Local Similarity 95.5%; Pred. No. 3.6e-42;
Matches 214; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 1 TATTCTTCTCTGATCTTCAGCAAGCTTCGGATTCTTCGAGCTGGTCTTTGGCATC 60
Db 574 TATTCTTCTCTGATCTTCAGCAAGCTTCAGATTCTCTTCGAGCTGGTCTTTGGCATC 633

QY 61 GAGCTGATGAAGTGAACCCATCGCCAGCTGTACATCTTTGCCACCTGCCCTGGCCCTC 120
Db 634 GAGCTGATGAAGTGAACCCATCGCCAGCTGTACATCTTTGCCACCTGCCCTGGCCCTC 693

QY 121 TCCTACGATGGCTGCTGGGTGACATCAGATCATG-CCCAGGACAGGCTTCCTGTATAAT 179
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